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        675              680              685

Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
    690              695              700

Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly
705              710              715              720

Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn
                725              730              735

Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
            740              745              750

Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val
        755              760              765

Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln
    770              775              780

Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu
785              790              795              800

Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala
            805              810              815

Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala
        820              825              830

Lys Gly His His His His His His
        835              840
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<210> 2814

<211> 2643

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2814
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ggaaagaaaa ttgccgttga tgctttcaac acgctatacc agttcatctc gataataagg   120

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cagcctgacg gtacgccgtt aaaggactca cagggcagaa tcacctctca cctttccgga      180

atcctataca gagtctccaa catggtcgag gtgggaatca ggccggtgtt tgtattcgac      240

ggagagccac cggagttcaa gaaggctgaa attgaggaga ggaaaaagag aagggctgag      300

gcagaggaga tgtggattgc ggctttgcag gcaggagata aggacgcgaa aaagtatgct      360

caggctgcag ggagggttga cgagtacatt gttgactccg caaagacgct tttaagttac      420

atggggattc cctttgtcga tgccccgtct gaaggagagg cgcaggctgc ttacatggca      480

gcaaaaggcg atgtggagta cacaggaagc caggattacg attctctgct cttcggaagc      540

ccgagactcg ccagaaatct cgcaataacg ggaaaaagga agcttcccgg caaaaatgtc      600

tatgtggatg taaagccgga gataataatt ctggaaagca acctcaaaag gctgggtttg      660

acgagggagc agctcatcga catagcgatt ctggtcggga cggactacaa tgagggtgtg      720

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gcactcaagg ctctgaaagt aaatattgac cacgtagagg agataaggaa tttcttcctg      840

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atcgagttcc tgtgcgagga gcacgacttc agcagggaga gggtcgagaa ggccttggag      960

aagctcaaag ctctgaagtc aacccaggcc acgcttgaga ggtggttcct ggaggaggcc     1020

ccctggcccc cgccggaagg ggccttcgtg ggcttcgtcc tctcccgccc cgagcccatg     1080

tgggcggagc ttaaagccct ggccgcctgc aggggcggcc gcgtgcaccg ggcagcagac     1140

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gtcttggcct cgagggaggg gctagacctc gtgcccgggg acgaccccat gctcctcgcc     1260

tacctcctgg ccccctcgaa caccacccccc gagggggtgg cgcggcgcta cgggggggag     1320

tggacggagg acgccgccca ccgggccctc ctctcggaga ggctccatcg gaacctcctt     1380

aagcgcctcg aggggggagga gaagctcctt tggctctacc acgaggtgga aaagcccctc     1440

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gcccttttccc tggagcttgc ggaggagatc cgccgcctcg aggaggaggt cttccgcttg     1560

gcgggccacc ccttcaacct caactcccgg gaccagctgg aaagggtgct cttttgacgag     1620

cttaggcttc ccgccttgaa gaagacgaag aagacaggca agcgctccac cagcgccgcg     1680

gtgctggagg ccctacggga ggcccacccc atcgtggaga gatcctcca gcaccgggag     1740

ctcaccaagc tcaagaacac ctacgtggac cccctcccaa gcctcgtcca cccgaggacg     1800

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ttcgtggccg aggcgggttg ggcgttggtg gccctggact atagccagat agagctccgc     1980
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ctctcccagg agcttgccat cccctacgag gaggcggtgg cctttataga gcgctacttc      2220

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aagagcgtca gggaggccgc ggagcgcatg gccttcaaca tgcccgtcca gggcaccgcc      2400

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gaggtggcgg ctttggccaa ggaggccatg gagaaggcct atcccctcgc cgtgcccctg      2580

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cac                                                                    2643


<210>  2815

<211>  881

<212>  PRT

<213>  Artificial Sequence


<220>

<223>  Synthetic

<400>  2815

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Glu Tyr Phe Ser Gly Lys Lys Ile Ala Val Asp Ala Phe Asn Thr Leu
                20                  25                  30


Tyr Gln Phe Ile Ser Ile Ile Arg Gln Pro Asp Gly Thr Pro Leu Lys
            35                  40                  45


Asp Ser Gln Gly Arg Ile Thr Ser His Leu Ser Gly Ile Leu Tyr Arg
        50                  55                  60


Val Ser Asn Met Val Glu Val Gly Ile Arg Pro Val Phe Val Phe Asp
65                  70                  75                  80


Gly Glu Pro Pro Glu Phe Lys Lys Ala Glu Ile Glu Glu Arg Lys Lys
```

Arg Arg Ala Glu Ala Glu Glu Met Trp Ile Ala Ala Leu Gln Ala Gly
        100   105   110

Asp Lys Asp Ala Lys Lys Tyr Ala Gln Ala Ala Gly Arg Val Asp Glu
        115   120   125

Tyr Ile Val Asp Ser Ala Lys Thr Leu Leu Ser Tyr Met Gly Ile Pro
    130   135   140

Phe Val Asp Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met Ala
145   150   155   160

Ala Lys Gly Asp Val Glu Tyr Thr Gly Ser Gln Asp Tyr Asp Ser Leu
           165   170   175

Leu Phe Gly Ser Pro Arg Leu Ala Arg Asn Leu Ala Ile Thr Gly Lys
        180   185   190

Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Asp Val Lys Pro Glu Ile
      195   200   205

Ile Ile Leu Glu Ser Asn Leu Lys Arg Leu Gly Leu Thr Arg Glu Gln
    210   215   220

Leu Ile Asp Ile Ala Ile Leu Val Gly Thr Asp Tyr Asn Glu Gly Val
225   230   235   240

Lys Gly Val Gly Val Lys Lys Ala Leu Asn Tyr Ile Lys Thr Tyr Gly
           245   250   255

Asp Ile Phe Arg Ala Leu Lys Ala Leu Lys Val Asn Ile Asp His Val
        260   265   270

Glu Glu Ile Arg Asn Phe Phe Leu Asn Pro Pro Val Thr Asp Asp Tyr
        275   280   285

Arg Ile Glu Phe Arg Glu Pro Asp Phe Glu Lys Ala Ile Glu Phe Leu
        290   295   300

Cys Glu Glu His Asp Phe Ser Arg Glu Arg Val Glu Lys Ala Leu Glu
305   310   315   320

Lys Leu Lys Ala Leu Lys Ser Thr Gln Ala Thr Leu Glu Arg Trp Phe
           325   330   335

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Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe
        340             345                 350

Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala
        355             360             365

Ala Cys Arg Gly Gly Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly
    370             375             380

Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala
385             390             395             400

Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro
            405             410             415

Met Leu Leu Ala Tyr Leu Leu Gly Pro Ser Asn Thr Thr Pro Glu Gly
        420             425             430

Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg
        435             440             445

Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu
    450             455             460

Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu
465             470             475             480

Ser Arg Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp Val
            485             490             495

Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg
        500             505             510

Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn
        515             520             525

Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro
    530             535             540

Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala
545             550             555             560

Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu
            565             570             575

Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu
        580             585             590
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Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn
        595   600   605

Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu
        610   615   620

Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala
625   630   635   640

Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln
            645   650   655

Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile
            660   665   670

Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp
        675   680   685

Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala
        690   695   700

Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg
705   710   715   720

Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile
            725   730   735

Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys
        740   745   750

Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly
        755   760   765

Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg
    770   775   780

Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala
785   790   795   800

Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg
            805   810   815

Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu
            820   825   830

Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu

Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val
    850   855   860

Gly Met Gly Glu Asp Trp Leu Ser Ala Lys Gly His His His His His
865   870   875   880

His

<210>   2816

<211>   2619

<212>   DNA

<213>   Artificial Sequence

<220>

<223>   Synthetic

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ggaaagaaaa ttgccgttga tgctttcaac acgctatacc agttcatctc gataataagg   120

cagcctgacg gtacgccgtt aaaggactca cagggcagaa tcacctctca cctttccgga   180

atcctataca gagtctccaa catggtcgag gtgggaatca ggccggtgtt tgtattcgac   240

ggagagccac cggagttcaa gaaggctgaa attgaggaga ggaaaaagag aagggctgag   300

gcagaggaga tgtggattgc ggctttgcag gcaggagata aggacgcgaa aaagtatgct   360

caggctgcag ggagggttga cgagtacatt gttgactccg caaagacgct tttaagttac   420

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gcaaaaggcg atgtggagta cacaggaagc caggattacg attctctgct cttcggaagc   540

ccgagactcg ccagaaatct cgcaataacg ggaaaaagga agcttcccgg caaaaatgtc   600

tatgtggatg taaagccgga gataataatt ctggaaagca acctcaaaag gctgggtttg   660

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gcactcaagg ctctgaaagt aaatattgac cacgtagagg agataaggaa tttcttcctg   840

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atcgagttcc tgtgcgagga gcacgacttc agcagggaga gggtcgagaa ggccttggag   960

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aaggaggtcc ggggcctcct cgccaaggac ctcgccgtct tggcctcgag ggaggggcta      1200

gacctcgtgc ccggggacga ccccatgctc ctcgcctacc tcctgggccc ctcgaacacc      1260

accccgagg gggtggcgcg gcgctacggg ggggagtgga cggaggacgc cgcccaccgg      1320

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ttggtggccc tggactatag ccagatagag ctccgcgtcc tcgcccacct ctccggggac      1980

gaaaacctga tcagggtctt ccaggagggg aaggacatcc acacccagac cgcaagctgg      2040

atgttcggcg tccccccgga ggccgtggac cccctgatgc gccgggcggc caagacggtg      2100

aacttcggcg tcctctacgg catgtccgcc cataggctct cccaggagct tgccatcccc      2160

tacgaggagg cggtggcctt tatagagcgc tacttccaaa gcttccccaa ggtgcgggcc      2220

tggatagaaa agaccctgga ggagggagg aagcggggct acgtggaaac cctcttcgga      2280

agaaggcgct acgtgcccga cctcaacgcc cgggtgaaga gcgtcaggga ggccgcggag      2340

cgcatggcct tcaacatgcc cgtccagggc accgccgccg acctcatgaa gctcgccatg      2400

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gccatggaga aggcctatcc cctcgccgtg cccctggagg tggaggtggg gatgggggag      2580

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<210> 2817

<211> 873

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2817

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Glu Tyr Phe Ser Gly Lys Lys Ile Ala Val Asp Ala Phe Asn Thr Leu
            20   25   30

Tyr Gln Phe Ile Ser Ile Ile Arg Gln Pro Asp Gly Thr Pro Leu Lys
        35   40   45

Asp Ser Gln Gly Arg Ile Thr Ser His Leu Ser Gly Ile Leu Tyr Arg
    50   55   60

Val Ser Asn Met Val Glu Val Gly Ile Arg Pro Val Phe Val Phe Asp
65   70   75   80

Gly Glu Pro Pro Glu Phe Lys Lys Ala Glu Ile Glu Glu Arg Lys Lys
            85   90   95

Arg Arg Ala Glu Ala Glu Glu Met Trp Ile Ala Ala Leu Gln Ala Gly
            100   105   110

Asp Lys Asp Ala Lys Lys Tyr Ala Gln Ala Ala Gly Arg Val Asp Glu
    115   120   125

Tyr Ile Val Asp Ser Ala Lys Thr Leu Leu Ser Tyr Met Gly Ile Pro
    130   135   140

Phe Val Asp Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met Ala
145   150   155   160

Ala Lys Gly Asp Val Glu Tyr Thr Gly Ser Gln Asp Tyr Asp Ser Leu
            165   170   175

Leu Phe Gly Ser Pro Arg Leu Ala Arg Asn Leu Ala Ile Thr Gly Lys
            180   185   190

Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Asp Val Lys Pro Glu Ile
    195   200   205

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Ile Ile Leu Glu Ser Asn Leu Lys Arg Leu Gly Leu Thr Arg Glu Gln
    210   215   220

Leu Ile Asp Ile Ala Ile Leu Val Gly Thr Asp Tyr Asn Glu Gly Val
225   230   235   240

Lys Gly Val Gly Val Lys Lys Ala Leu Asn Tyr Ile Lys Thr Tyr Gly
            245   250   255

Asp Ile Phe Arg Ala Leu Lys Ala Leu Lys Val Asn Ile Asp His Val
            260   265   270

Glu Glu Ile Arg Asn Phe Phe Leu Asn Pro Pro Val Thr Asp Asp Tyr
            275   280   285

Arg Ile Glu Phe Arg Glu Pro Asp Phe Glu Lys Ala Ile Glu Phe Leu
    290   295   300

Cys Glu Glu His Asp Phe Ser Arg Glu Arg Val Glu Lys Ala Leu Glu
305   310   315   320

Lys Leu Lys Ala Leu Lys Ser Thr Leu Glu Glu Ala Pro Trp Pro Pro
            325   330   335

Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met
            340   345   350

Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His
    355   360   365

Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg
    370   375   380

Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu
385   390   395   400

Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Gly
            405   410   415

Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu
            420   425   430

Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His
    435   440   445

Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu
    450   455   460

Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu
465   470   475   480

Ala Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu
            485   490   495

Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu
            500   505   510

Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val
            515   520   525

Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr
    530   535   540

Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala
545   550   555   560

His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu
            565   570   575

Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr
            580   585   590

Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg
            595   600   605

Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro
    610   615   620

Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala
625   630   635   640

Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His
            645   650   655

Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp
            660   665   670

Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala
    675   680   685

Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val
    690   695   700

Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro

Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro
                725   730   735

Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg
                740   745   750

Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu
                755   760   765

Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe
    770   775   780

Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met
785   790   795   800

Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu
                805   810   815

Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu
                820   825   830

Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu
                835   840   845

Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser
    850   855   860

Ala Lys Gly His His His His His His
865   870

<210> 2818

<211> 2445

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2818
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taccgggccc tgaccggggа cgagtccgac aaccttcccg gggtcaaggg catcggggag     600

aagacggcga ggaagcttct ggaggagtgg gggagcctgg aagccctcct caagaacctg     660

gaccggctga gcccgccat ccgggagaag atcctggccc acatggacga tctgaagctc     720

tcctgggacc tggccaaggt gcgcaccgac ctgcccctgg aggtggactt cgccaaaagg     780

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ctggccgcct gcaggggcgg ccgcgtgcac cgggcagcag accccttggc ggggctaaag     960

gacctcaagg aggtccgggg cctcctcgcc aaggacctcg ccgtcttggc ctcgagggag    1020

gggctagacc tcgtgcccgg ggacgacccc atgctcctcg cctacctcct gggcccctcg    1080

aacaccaccc ccgaggggt ggcgcggcgc tacggggggg agtggacgga ggacgccgcc    1140

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gaggcccacc ccatcgtgga gaagatcctc cagcaccggg agctcaccaa gctcaagaac    1560

acctacgtgg accccctccc aagcctcgtc cacccgagga cgggccgcct ccacacccgc    1620

ttcaaccaga cggccacggc cacggggagg cttagtagct ccgaccccaa cctgcagaac    1680

atccccgtcc gcaccccctt gggccagagg atccgccggg ccttcgtggc cgaggcgggt    1740

tgggcgttgg tggccctgga ctatagccag atagagctcc gcgtcctcgc ccacctctcc    1800

ggggacgaaa acctgatcag ggtcttccag gaggggaagg acatccacac ccagaccgca    1860

agctggatgt tcggcgtccc cccggaggcc gtggaccccc tgatgcgccg ggcggccaag    1920

acggtgaact tcggcgtcct ctacggcatg tccgcccata ggctctccca ggagcttgcc    1980
```

```
atcccctacg aggaggcggt ggcctttata gagcgctact tccaaagctt ccccaaggtg    2040

cgggcctgga tagaaaagac cctggaggag gggaggaagc ggggctacgt ggaaaccctc    2100

ttcggaagaa ggcgctacgt gcccgacctc aacgcccggg tgaagagcgt cagggaggcc    2160

gcggagcgca tggccttcaa catgcccgtc cagggcaccg ccgccgacct catgaagctc    2220

gccatggtga agctcttccc ccgcctccgg gagatggggg cccgcatgct cctccaggtc    2280

gccaacgagc tcctcctgga ggcccccccaa gcgcgggccg aggaggtggc ggctttggcc    2340

aaggaggcca tggagaaggc ctatcccctc gccgtgcccc tggaggtgga ggtggggatg    2400

ggggaggact ggctttccgc caagggtcac caccaccacc accac                     2445
```

<210> 2819

<211> 815

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2819

```
Met Asn Ser Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val
1               5                   10                  15

Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu
            20                  25                  30

Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
        35                  40                  45

Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val
    50                  55                  60

Phe Asp Ala Lys Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr
65                  70                  75                  80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
                85                  90                  95

Leu Ile Lys Glu Met Val Asp Leu Leu Gly Leu Glu Arg Leu Glu Val
            100                 105                 110

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
```

- 2014 -

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu
    130   135   140

Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr
145   150   155   160

Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp
                165   170   175

Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu
            180   185   190

Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu
            195   200   205

Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys
    210   215   220

Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu
225   230   235   240

Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp
                245   250   255

Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Glu Lys Pro Arg Glu
            260   265   270

Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu
            275   280   285

Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys
    290   295   300

Arg Gly Gly Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys
305   310   315   320

Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu
                325   330   335

Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu
            340   345   350

Leu Ala Tyr Leu Leu Gly Pro Ser Asn Thr Thr Pro Glu Gly Val Ala
            355   360   365

```
Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu
    370             375             380
```

```
Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu
385             390             395             400
```

```
Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg
            405             410             415
```

```
Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp Val Ala Tyr
            420             425             430
```

```
Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu
        435             440             445
```

```
Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg
    450             455             460
```

```
Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu
465             470             475             480
```

```
Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu
            485             490             495
```

```
Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His
            500             505             510
```

```
Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser
        515             520             525
```

```
Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr
    530             535             540
```

```
Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn
545             550             555             560
```

```
Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val
            565             570             575
```

```
Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu
            580             585             590
```

```
Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val
        595             600             605
```

```
Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe
    610             615             620
```

Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys
625   630   635   640

Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser
            645   650   655

Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg
            660   665   670

Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu
        675   680   685

Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg
    690   695   700

Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala
705   710   715   720

Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp
            725   730   735

Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met
            740   745   750

Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala
        755   760   765

Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met
    770   775   780

Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Met
785   790   795   800

Gly Glu Asp Trp Leu Ser Ala Lys Gly His His His His His His
            805   810   815

<210>   2820

<211>   2520

<212>   DNA

<213>   Artificial Sequence

<220>

<223>   Synthetic

<400> 2820

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ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc     120

gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct caaggaggac     180

ggggacgcgg tgatcgtggt cttttgacgcc aaggcccccct ccttccgcca cgaggcctac    240

gggggtaca aggcgggccg gcccccacc ccggaggact cccccgccca gctcgccttg      300

gtcaagcggc tggtggacct tctgggcctg gtccgcctcg aggccccggg gtacgaggcg     360

gacgacgtcc tgggcaccct ggccaagaag gccgaaaagg aggggtacga ggtgcgcatc     420

ctcaccgccg accgcgacct ctaccaactc gtctccgacc gcatccacgt cctccacccc     480

gaggggtacc tcatcacccc ggagtggctt tgggagaagt atgggcttaa gccttcccag     540

tgggtggact accgggcctt ggccggggac ccttccgaca catccccgg cgtgaagggc      600

atcgggagga agacggcggc caagctgatc cgggagtggg gaagcctgga aaacctcctc     660

aagaacctgg accggctgaa gcccgccatc cgggagaaga tcctggccca catggacgat     720

ctgaagctct cctgggacct ggccaaggtg cgcaccgacc tgcccctgga ggtggacttc     780

gccaaaaggc gggagcccga ccgggagagg cttagggcct ttctggagag gcttgagttt     840

ggcagcctcc tccacgagtt cggccttctg aaagccccca aggccctgga ggaggccccc     900

tggccccccgc cggaagggggc cttcgtgggc ttcgtcctct cccgccccga gcccatgtgg    960

gcggagctta aagccctggc cgcctgcagg ggcggccgcg tgcaccgggc agcagacccc    1020

ttggcggggc taaaggacct caaggaggtc cggggcctcc tcgccaagga cctcgccgtc    1080

ttggcctcga gggagggggct agacctcgtg cccggggacg accccatgct cctcgcctac    1140

ctcctgggcc cctcgaacac caccccccgag ggggtggcgc ggcgctacgg ggggagtgg    1200

acggaggacg ccgcccaccg ggccctcctc tcggagaggc tccatcggaa cctccttaag    1260

cgcctcgagg gggaggagaa gctcctttgg ctctaccacg aggtggaaaa gcccctctcc    1320

cgggtcctgg cccatatgga ggccaccggg gtacggctgg acgtggccta ccttcaggcc    1380

ctttcccctgg agcttgcgga ggagatccgc cgcctcgagg aggaggtctt ccgcttggcg    1440

ggccacccct tcaacctcaa ctcccgggac cagctggaaa gggtgctctt tgacgagctt    1500

aggcttcccg ccttgaagaa gacgaagaag acaggcaagc gctccaccag cgccgcggtg    1560

ctggaggccc tacgggaggc ccaccccatc gtggagaaga tcctccagca ccgggagctc    1620

accaagctca gaacaccta cgtggacccc ctcccaagcc tcgtccaccc gaggacgggc    1680

cgcctccaca cccgcttcaa ccagacggcc acggccacgg ggaggcttag tagctccgac    1740

cccaacctgc agaacatccc cgtccgcacc cccttgggcc agaggatccg ccgggccttc    1800

gtggccgagg cgggttgggc gttggtggcc ctggactata gccagataga gctccgcgtc    1860
```

- 2018 -

ctcgcccacc tctccgggga cgaaaacctg atcagggtct tccaggaggg gaaggacatc   1920

cacacccaga ccgcaagctg gatgttcggc gtccccccgg aggccgtgga ccccctgatg   1980

cgccgggcgg ccaagacggt gaacttcggc gtcctctacg gcatgtccgc ccataggctc   2040

tcccaggagc ttgccatccc ctacgaggag gcggtggcct ttatagagcg ctacttccaa   2100

agcttcccca aggtgcgggc ctggatagaa aagaccctgg aggaggggag gaagcggggc   2160

tacgtggaaa ccctcttcgg aagaaggcgc tacgtgcccg acctcaacgc ccgggtgaag   2220

agcgtcaggg aggccgcgga gcgcatggcc ttcaacatgc ccgtccaggg caccgccgcc   2280

gacctcatga agctcgccat ggtgaagctc ttcccccgcc tccgggagat ggggggcccgc   2340

atgctcctcc aggtcgccaa cgagctcctc ctggaggccc cccaagcgcg ggccgaggag   2400

gtggcggctt tggccaagga ggccatggag aaggcctatc ccctcgccgt gcccctggag   2460

gtggaggtgg ggatggggga ggactggctt tccgccaagg gtcaccacca ccaccaccac   2520

<210> 2821

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2821

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1   5   10   15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
            20   25   30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
        35   40   45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val
    50   55   60

Ile Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr
65   70   75   80

Gly Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg
                85   90   95

- 2019 -

Gln Leu Ala Leu Val Lys Arg Leu Val Asp Leu Leu Gly Leu Val Arg
        100   105   110

Leu Glu Ala Pro Gly Tyr Glu Ala Asp Asp Val Leu Gly Thr Leu Ala
        115   120   125

Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp
        130   135   140

Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Ile His Val Leu His Pro
145   150   155   160

Glu Gly Tyr Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu
            165   170   175

Lys Pro Ser Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser
            180   185   190

Asp Asn Ile Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala Lys
        195   200   205

Leu Ile Arg Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp
        210   215   220

Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp
225   230   235   240

Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu
            245   250   255

Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg
            260   265   270

Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
        275   280   285

Leu Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro
        290   295   300

Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp
305   310   315   320

Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg
            325   330   335

Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly
            340   345   350

- 2020 -

```
Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp
        355              360              365

Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Gly Pro
    370              375              380

Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp
385              390              395              400

Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg
                405              410              415

Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr
            420              425              430

His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
        435              440              445

Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu
    450              455              460

Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala
465              470              475              480

Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
            485              490              495

Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly
        500              505              510

Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His
        515              520              525

Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys
    530              535              540

Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly
545              550              555              560

Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
            565              570              575

Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu
            580              585              590

Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu
```

- 2021 -

Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
    610   615   620

Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile
625   630   635   640

His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val
                645   650   655

Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
            660   665   670

Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr
            675   680   685

Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
    690   695   700

Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly
705   710   715   720

Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn
                725   730   735

Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
            740   745   750

Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val
            755   760   765

Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln
    770   775   780

Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu
785   790   795   800

Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala
                805   810   815

Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala
            820   825   830

Lys Gly His His His His His His
    835   840

<210> 2822

<211> 2445

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2822
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caggcggtgt acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg     180

gtgatcgtgg tgtttgacgc caaggccccc tccttccgcc accagaccta cgaggcctac     240

aaggcggggc gggctcccac ccccgaggac tttccccggc agcttgccct tatcaaggag     300

atggtggacc ttttgggctt tacccgcctc gaggtgccgg gctttgaagc ggatgacgtc     360

ctggctaccc tggccaagaa ggcggaaaag gagggctacg aggtccgcat cctcaccgcc     420

gacaaagacc tttaccagct cctttccgac cgcatccacg tcctccaccc cgagggggtac     480

ctcatcaccc cggcctggct ttgggaaaag tacggcctga ggcccgacca gtgggccgac     540

taccgggccc tgaccgggga cgagtccgac aaccttcccg gggtcaaggg catcggggag     600

aagacggcga ggaagcttct ggaggagtgg gggagcctgg aagccctcct caagaacctg     660

gaccggctga gcccgccat ccgggagaag atcctggccc acatggacga tctgaagctc     720

tcctgggacc tggccaaggt gcgcaccgac ctgcccctgg aggtggactt cgccaaaagg     780

cgggagcccg accgggaggg ggagaagccc cgggaggagg cccccctggcc cccgcccgaa     840

ggggccttcg tgggcttcct cctttcccgc cccgagccca tgtgggcgga gcttaaagcc     900

ctggccgcct gcaggggcgg ccgcgtgcac cgggcagcag accccttggc ggggctaaag     960

gacctcaagg aggtccgggg cctcctcgcc aaggacctcg ccgtcttggc ctcgagggag    1020

gggctagacc tcgtgcccgg ggacgacccc atgctcctcg cctacctcct gggcccctcg    1080

aacaccaccc ccgaggggggt ggcgcggcgc tacggggggg agtggacgga ggacgccgcc    1140

caccgggccc tcctctcgga gaggctccat cggaacctcc ttaagcgcct cgaggggggag    1200

gagaagctcc tttggctcta ccacgaggtg gaaaagcccc tctcccgggt cctggcccat    1260

atggaggcca ccggggtacg gctggacgtg gcctaccttc aggccctttc cctggagctt    1320

gcggaggaga tccgccgcct cgaggaggag gtcttccgct ggcgggccca ccccttcaac    1380

ctcaactccc gggaccagct ggaaagggtg ctctttgacg agcttaggct tcccgccttg    1440
```

aagaagacga agaagacagg caagcgctcc accagcgccg cggtgctgga ggccctacgg   1500

gaggcccacc ccatcgtgga gaagatcctc cagcaccggg agctcaccaa gctcaagaac   1560

acctacgtgg accccctccc aagcctcgtc cacccgagga cgggccgcct ccacacccgc   1620

ttcaaccaga cggccacggc cacggggagg cttagtagct ccgaccccaa cctgcagaac   1680

atccccgtcc gcaccccctt gggccagagg atccgccggg ccttcgtggc cgaggcgggt   1740

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ggggacgaaa acctgatcag ggtcttccag gaggggaagg acatccacac ccagaccgca   1860

agctggatgt tcggcgtccc cccggaggcc gtggacccccc tgatgcgccg ggcggccaag   1920

acggtgaact tcggcgtcct ctacggcatg tccgcccata ggctctccca ggagcttgcc   1980

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cgggcctgga tagaaaagac cctggaggag gggaggaagc ggggctacgt ggaaaccctc   2100

ttcggaagaa ggcgctacgt gcccgacctc aacgcccggg tgaagagcgt cagggaggcc   2160

gcggagcgca tggccttcaa catgcccgtc cagggcaccg ccgccgacct catgaagctc   2220

gccatggtga agctcttccc ccgcctccgg gagatggggg cccgcatgct cctccaggtc   2280

gccaacgagc tcctcctgga ggcccccccaa gcgcgggccg aggaggtggc ggctttggcc   2340

aaggaggcca tggagaaggc ctatcccctc gccgtgcccc tggaggtgga ggtgggggatg   2400

ggggaggact ggctttccgc caagggtcac caccaccacc accac   2445

<210>   2823

<211>   815

<212>   PRT

<213>   Artificial Sequence

<220>

<223>   Synthetic

<400>   2823

Met Asn Ser Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val
1   5   10   15

Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu
                20   25   30

Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
            35   40   45

- 2024 -

```
Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val
    50              55              60

Phe Asp Ala Lys Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr
65              70              75                      80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
            85              90                      95

Leu Ile Lys Glu Met Val Asp Leu Leu Gly Phe Thr Arg Leu Glu Val
            100             105             110

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
            115             120             125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu
    130             135             140

Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr
145             150             155             160

Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp
            165             170             175

Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu
            180             185             190

Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu
            195             200             205

Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys
    210             215             220

Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu
225             230             235             240

Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp
            245             250             255

Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Glu Lys Pro Arg Glu
            260             265             270

Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu
            275             280             285

Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys
    290             295             300

                          - 2025 -
```

Arg Gly Gly Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys
305   310   315   320

Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu
            325   330   335

Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu
            340   345   350

Leu Ala Tyr Leu Leu Gly Pro Ser Asn Thr Thr Pro Glu Gly Val Ala
            355   360   365

Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu
    370   375   380

Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu
385   390   395   400

Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg
            405   410   415

Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp Val Ala Tyr
            420   425   430

Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu
            435   440   445

Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg
    450   455   460

Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu
465   470   475   480

Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu
            485   490   495

Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His
            500   505   510

Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser
    515   520   525

Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr
    530   535   540

Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn

```
        545                    550                    555                    560

Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val
            565                 570                 575

Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu
            580                 585                 590

Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val
            595                 600                 605

Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe
    610                 615                 620

Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys
625                 630                 635                 640

Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser
            645                 650                 655

Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg
            660                 665                 670

Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu
            675                 680                 685

Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg
            690                 695                 700

Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala
705                 710                 715                 720

Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp
            725                 730                 735

Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met
            740                 745                 750

Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala
            755                 760                 765

Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met
    770                 775                 780

Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Met
785                 790                 795                 800
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Gly Glu Asp Trp Leu Ser Ala Lys Gly His His His His His His
        805   810   815

<210> 2824

<211> 2520

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2824
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gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct caaggaggac   180

ggggacgcgg tgatcgtggt ctttgacgcc aaggcccct ccttccgcca cgaggcctac   240

ggggggtaca aggcgggccg ggcccccacc ccggaggact cccccgcca gctcgccttg   300

gtcaagcggc tggtggacct tctgggcttt acccgcctcg aggccccggg gtacgaggcg   360

gacgacgtcc tgggcaccct ggccaagaag gccgaaaagg aggggtacga ggtgcgcatc   420

ctcaccgccg accgcgacct ctaccaactc gtctccgacc gcatccacgt cctccacccc   480

gaggggtacc tcatcacccc ggagtggctt tgggagaagt atgggcttaa gccttcccag   540

tgggtggact accgggcctt ggccggggac ccttccgaca catccccgg cgtgaagggc   600

atcggggaga agacggcggc caagctgatc cgggagtggg gaagcctgga aaacctcctc   660

aagaacctgg accggctgaa gcccgccatc cgggagaaga tcctggccca catggacgat   720

ctgaagctct cctgggacct ggccaaggtg cgcaccgacc tgcccctgga ggtggacttc   780

gccaaaaggc gggagcccga ccgggagagg cttagggcct ttctggagag gcttgagttt   840

ggcagcctcc tccacgagtt cggccttctg aaagccccca aggccctgga ggaggccccc   900

tggcccccgc cggaaggggc cttcgtgggc ttcgtcctct cccgcccga gcccatgtgg   960

gcggagctta agcccctggc cgcctgcagg ggcggccgcg tgcaccgggc agcagacccc 1020

ttggcggggc taaaggacct caaggaggtc cggggcctcc tcgccaagga cctcgccgtc 1080

ttggcctcga gggaggggct agacctcgtg cccggggacg accccatgct cctcgcctac 1140

ctcctgggcc cctcgaacac caccccgag ggggtggcgc ggcgctacgg ggggagtgg 1200

acggaggacg ccgcccaccg ggccctcctc tcggagaggc tccatcggaa cctccttaag 1260

cgcctcgagg gggaggagaa gctcctttgg ctctaccacg aggtggaaaa gcccctctcc 1320

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ctttccctgg agcttgcgga ggagatccgc cgcctcgagg aggaggtctt ccgcttggcg   1440

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cgcctccaca cccgcttcaa ccagacggcc acggccacgg ggaggcttag tagctccgac   1740

cccaacctgc agaacatccc cgtccgcacc cccttgggcc agaggatccg ccgggccttc   1800

gtggccgagg cgggttgggc gttggtggcc ctggactata gccagataga gctccgcgtc   1860

ctcgcccacc tctccgggga cgaaaacctg atcagggtct ccaggagggg aaggacatc   1920

cacacccaga ccgcaagctg gatgttcggc gtccccccgg aggccgtgga ccccctgatg   1980

cgccgggcgg ccaagacggt gaacttcggc gtcctctacg gcatgtccgc ccataggctc   2040

tcccaggagc ttgccatccc ctacgaggag gcggtggcct ttatagagcg ctacttccaa   2100

agcttcccca aggtgcgggc ctggatagaa aagaccctgg aggagggggag gaagcggggc   2160

tacgtggaaa ccctcttcgg aagaaggcgc tacgtgcccg acctcaacgc ccgggtgaag   2220

agcgtcaggg aggccgcgga gcgcatggcc ttcaacatgc ccgtccaggg caccgccgcc   2280

gacctcatga gctcgccat ggtgaagctc ttccccccgcc tccgggagat ggggggcccgc   2340

atgctcctcc aggtcgccaa cgagctcctc ctggaggccc cccaagcgcg ggccgaggag   2400

gtggcggctt tggccaagga ggccatggag aaggcctatc ccctcgccgt gccctggag   2460

gtggaggtgg ggatgggggga ggactggctt tccgccaagg gtcaccacca ccaccaccac   2520
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<210> 2825

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2825

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Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1               5                   10                  15


Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
```

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
        35   40   45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val
    50   55   60

Ile Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr
65   70   75   80

Gly Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg
            85   90   95

Gln Leu Ala Leu Val Lys Arg Leu Val Asp Leu Leu Gly Phe Thr Arg
        100   105   110

Leu Glu Ala Pro Gly Tyr Glu Ala Asp Asp Val Leu Gly Thr Leu Ala
    115   120   125

Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp
    130   135   140

Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Ile His Val Leu His Pro
145   150   155   160

Glu Gly Tyr Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu
            165   170   175

Lys Pro Ser Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser
            180   185   190

Asp Asn Ile Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala Lys
        195   200   205

Leu Ile Arg Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp
    210   215   220

Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp
225   230   235   240

Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu
            245   250   255

Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg
            260   265   270

                                                    .

```
Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
        275                 280                 285

Leu Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro
        290                 295                 300

Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp
305                 310                 315                 320

Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg
                325                 330                 335

Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly
            340                 345                 350

Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp
        355                 360                 365

Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Gly Pro
    370                 375                 380

Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp
385                 390                 395                 400

Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg
                405                 410                 415

Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr
            420                 425                 430

His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
        435                 440                 445

Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu
    450                 455                 460

Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala
465                 470                 475                 480

Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
            485                 490                 495

Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly
            500                 505                 510

Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His
        515                 520                 525
```

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Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys
    530                 535                 540

Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly
545                 550                 555                 560

Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
                565                 570                 575

Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu
            580                 585                 590

Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu
            595                 600                 605

Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
    610                 615                 620

Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile
625                 630                 635                 640

His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val
                645                 650                 655

Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
            660                 665                 670

Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr
            675                 680                 685

Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
    690                 695                 700

Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly
705                 710                 715                 720

Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn
                725                 730                 735

Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
            740                 745                 750

Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val
            755                 760                 765

Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln
```

Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu
785   790   795   800

Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala
                    805   810   815

Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala
                    820   825   830

Lys Gly His His His His His His
              835   840

<210> 2826

<211> 2445

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2826
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ctggcctacc gtaccttttt tgccctgaag ggcctcacca ccagccgcgg ggagccggtc   120

caggcggtgt acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg   180

gtgatcgtgg tctttgacgc cgaggccccc tccttccgcc accagaccta cgaggcctac   240

aaggcggggc gggctcccac ccccgaggac tttccccggc agcttgccct tatcaaggag   300

atggtggacc ttttgggcct ggagcgcctc gaggtgccgg gctttgaagc ggatgacgtc   360

ctggctaccc tggccaagaa ggcggaaaag gagggctacg aggtccgcat cctcaccgcc   420

gacaaagacc tttaccagct cctttccgac cgcatccacg tcctccaccc cgagggggtac   480

ctcatcaccc cggcctggct ttgggaaaag tacggcctga ggcccgacca gtgggccgac   540

taccgggccc tgaccgggga cgagtccgac aaccttcccg gggtcaaggg catcggggag   600

aagacggcga ggaagcttct ggaggagtgg gggagcctgg aagccctcct caagaacctg   660

gaccggctga gcccgccat ccgggagaag atcctggccc acatggacga tctgaagctc   720

tcctgggacc tggccaaggt gcgcaccgac ctgcccctgg aggtggactt cgccaaaagg   780

cgggagcccg accgggaggg ggagaagccc cgggaggagg cccctggcc cccgcccgaa   840

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ggggccttcg tgggcttcct cctttcccgc cccgagccca tgtgggcgga gcttaaagcc      900

ctggccgcct gcaggggcgg ccgcgtgcac cgggcagcag acccccttggc ggggctaaag     960

gacctcaagg aggtccgggg cctcctcgcc aaggacctcg ccgtcttggc ctcgagggag      1020

gggctagacc tcgtgcccgg ggacgacccc atgctcctcg cctacctcct gggcccctcg      1080

aacaccaccc ccgagggggt ggcgcggcgc tacggggggg agtggacgga ggacgccgcc      1140

caccgggccc tcctctcgga gaggctccat cggaacctcc ttaagcgcct cgaggggag      1200

gagaagctcc tttggctcta ccacgaggtg gaaaagcccc tctcccgggt cctggcccat     1260

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gaggcccacc ccatcgtgga gaagatcctc cagcaccggg agctcaccaa gctcaagaac    1560

acctacgtgg accccctccc aagcctcgtc cacccgagga cgggccgcct ccacacccgc     1620

ttcaaccaga cggccacggc cacgggggagg cttagtagct ccgaccccaa cctgcagaac   1680

atccccgtcc gcaccccctt gggccagagg atccgccggg ccttcgtggc cgaggcgggt    1740

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agctggatgt tcggcgtccc cccggaggcc gtggaccccc tgatgcgccg ggcggccaag     1920

acggtgaact tcggcgtcct ctacggcatg tccgcccata ggctctccca ggagcttgcc     1980

atcccctacg aggaggcggt ggcctttata gagcgctact tccaaagctt ccccaaggtg    2040

cgggcctgga tagaaaagac cctggaggag gggaggaagc ggggctacgt ggaaaccctc     2100

ttcggaagaa ggcgctacgt gcccgacctc aacgcccggg tgaagagcgt cagggaggcc    2160

gcggagcgca tggccttcaa catgcccgtc cagggcaccg ccgccgacct catgaagctc     2220

gccatggtga agctcttccc ccgcctccgg gagatggggg cccgcatgct cctccaggtc    2280

gccaacgagc tcctcctgga ggcccccaa gcgcgggccg aggaggtggc ggctttggcc     2340

aaggaggcca tggagaaggc ctatcccctc gccgtgcccc tggaggtgga ggtgggggatg   2400

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<210>  2827

<211>  815

<212>  PRT

<213>  Artificial Sequence
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<220>

<223> Synthetic

<400> 2827

Met Asn Ser Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val
1   5   10   15

Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu
                20   25   30

Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
            35   40   45

Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val
        50   55   60

Phe Asp Ala Glu Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr
65   70   75   80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
                85   90   95

Leu Ile Lys Glu Met Val Asp Leu Leu Gly Leu Glu Arg Leu Glu Val
                100   105   110

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
            115   120   125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu
    130   135   140

Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr
145   150   155   160

Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp
                165   170   175

Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu
                180   185   190

Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu
            195   200   205

Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys
    210   215   220

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Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu
225   230   235   240

Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp
                245   250   255

Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Glu Lys Pro Arg Glu
            260   265   270

Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu
            275   280   285

Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys
        290   295   300

Arg Gly Gly Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys
305   310   315   320

Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu
            325   330   335

Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu
            340   345   350

Leu Ala Tyr Leu Leu Gly Pro Ser Asn Thr Thr Pro Glu Gly Val Ala
            355   360   365

Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu
            370   375   380

Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu
385   390   395   400

Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg
                405   410   415

Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp Val Ala Tyr
            420   425   430

Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu
            435   440   445

Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg
    450   455   460

Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu

Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu
            485   490   495

Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His
            500   505   510

Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser
            515   520   525

Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr
    530   535   540

Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn
545   550   555   560

Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val
            565   570   575

Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu
            580   585   590

Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val
            595   600   605

Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe
    610   615   620

Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys
625   630   635   640

Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser
            645   650   655

Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg
            660   665   670

Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu
    675   680   685

Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg
    690   695   700

Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala
705   710   715   720

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Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp
            725             730              735

Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met
            740             745              750

Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala
            755             760              765

Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met
        770             775              780

Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Met
785             790             795              800

Gly Glu Asp Trp Leu Ser Ala Lys Gly His His His His His His
                805             810              815
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<210> 2828

<211> 2445

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

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<400> 2828
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caggcggtgt acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg   180
gtgatcgtgg tctttgacgc cgaggccccc tccttccgcc accagaccta cgaggcctac   240
aaggcggggc gggctcccac ccccgaggac tttccccggc agcttgccct tatcaaggag   300
atggtggacc ttttgggctt tacccgcctc gaggtgccgg gctttgaagc ggatgacgtc   360
ctggctaccc tggccaagaa ggcggaaaag gagggctacg aggtccgcat cctcaccgcc   420
gacaaagacc tttaccagct ccttttccgac cgcatccacg tcctccaccc cgagggggtac   480
ctcatcaccc cggcctggct ttgggaaaag tacggcctga ggcccgacca gtgggccgac   540
taccgggccc tgaccgggga cgagtccgac aaccttcccg gggtcaaggg catcggggag   600
aagacggcga ggaagcttct ggaggagtgg gggagcctgg aagcccctcct caagaacctg   660
gaccggctga gcccgccat ccgggagaag atcctggccc acatggacga tctgaagctc   720
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tcctgggacc tggccaaggt gcgcaccgac ctgcccctgg aggtggactt cgccaaaagg    780

cgggagcccg accgggaggg ggagaagccc cgggaggagg cccccctggcc cccgcccgaa    840

ggggccttcg tgggcttcct cctttcccgc cccgagccca tgtgggcgga gcttaaagcc    900

ctggccgcct gcaggggcgg ccgcgtgcac cgggcagcag accccttggc ggggctaaag    960

gacctcaagg aggtccgggg cctcctcgcc aaggacctcg ccgtcttggc ctcgagggag    1020

gggctagacc tcgtgcccgg ggacgacccc atgctcctcg cctacctcct gggcccctcg    1080

aacaccaccc ccgaggggt ggcgcggcgc tacgggggg agtggacgga ggacgccgcc       1140

caccgggccc tcctctcgga gaggctccat cggaacctcc ttaagcgcct cgagggggag    1200

gagaagctcc tttggctcta ccacgaggtg gaaaagcccc tctcccgggt cctggcccat    1260

atggaggcca ccggggtacg gctggacgtg gcctaccttc aggcccttc cctggagctt     1320

gcggaggaga tccgccgcct cgaggaggag gtcttccgct tggcgggcca ccccttcaac    1380

ctcaactccc gggaccagct ggaaagggtg ctctttgacg agcttaggct tcccgccttg    1440

aagaagacga agaagacagg caagcgctcc accagcgccg cggtgctgga ggccctacgg    1500

gaggcccacc ccatcgtgga gaagatcctc cagcaccggg agctcaccaa gctcaagaac    1560

acctacgtgg accccctccc aagcctcgtc cacccgagga cgggccgcct ccacacccgc    1620

ttcaaccaga cggccacggc cacggggagg cttagtagct ccgaccccaa cctgcagaac    1680

atccccgtcc gcaccccctt gggccagagg atccgccggg ccttcgtggc cgaggcgggt    1740

tgggcgttgg tggccctgga ctatagccag atagagctcc gcgtcctcgc ccacctctcc    1800

ggggacgaaa acctgatcag ggtcttccag gaggggaagg acatccacac ccagaccgca    1860

agctggatgt tcggcgtccc cccggaggcc gtggaccccc tgatgcgccg ggcggccaag    1920

acggtgaact tcggcgtcct ctacggcatg tccgcccata ggctctccca ggagcttgcc    1980

atccctacg aggaggcggt ggcctttata gagcgctact tccaaagctt ccccaaggtg     2040

cgggcctgga tagaaaagac cctggaggag gggaggaagc ggggctacgt ggaaaccctc    2100

ttcggaagaa ggcgctacgt gcccgacctc aacgcccggg tgaagagcgt cagggaggcc    2160

gcggagcgca tggccttcaa catgcccgtc cagggcaccg ccgccgacct catgaagctc    2220

gccatggtga agctcttccc ccgcctccgg gagatggggg cccgcatgct cctccaggtc    2280

gccaacgagc tcctcctgga ggcccccaa gcgcgggccg aggaggtggc ggctttggcc     2340

aaggaggcca tggagaaggc ctatcccctc gccgtgcccc tggaggtgga ggtggggatg    2400

ggggaggact ggctttccgc caagggtcac caccaccacc accac                     2445
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<210> 2829

<211> 815

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2829

Met Asn Ser Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val
1   5   10   15

Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu
            20   25   30

Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
        35   40   45

Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val
    50   55   60

Phe Asp Ala Glu Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr
65   70   75   80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
                85   90   95

Leu Ile Lys Glu Met Val Asp Leu Leu Gly Phe Thr Arg Leu Glu Val
            100   105   110

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
            115   120   125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu
    130   135   140

Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr
145   150   155   160

Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp
                165   170   175

Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu
                180   185   190

Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu
            195   200   205

Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys
    210   215   220

Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu
225   230   235   240

Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp
            245   250   255

Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Glu Lys Pro Arg Glu
            260   265   270

Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu
        275   280   285

Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys
    290   295   300

Arg Gly Gly Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys
305   310   315   320

Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu
            325   330   335

Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu
            340   345   350

Leu Ala Tyr Leu Leu Gly Pro Ser Asn Thr Thr Pro Glu Gly Val Ala
        355   360   365

Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu
    370   375   380

Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu
385   390   395   400

Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg
            405   410   415

Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp Val Ala Tyr
            420   425   430

Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu
        435   440   445

Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg

```
        450                    455                    460


Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu
465                    470                    475                    480


Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu
                   485                    490                    495


Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His
              500                    505                    510


Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser
              515                    520                    525


Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr
         530                    535                    540


Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn
545                    550                    555                    560


Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val
              565                    570                    575


Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu
         580                    585                    590


Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val
         595                    600                    605


Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe
         610                    615                    620


Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys
625                    630                    635                    640


Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser
              645                    650                    655


Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg
         660                    665                    670


Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu
         675                    680                    685


Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg
         690                    695                    700


                              - 2042 -
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Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala
705             710         715             720

Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp
            725             730             735

Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met
            740             745             750

Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala
            755             760             765

Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met
    770             775             780

Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Met
785             790             795             800

Gly Glu Asp Trp Leu Ser Ala Lys Gly His His His His His His
            805             810             815


<210>   2830

<211>   2520

<212>   DNA

<213>   Artificial Sequence


<220>

<223>   Synthetic

<400>   2830
atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac      60

ggccaccacc tggcctaccg tacctttttt gccctgaagg gcctcaccac cagccggggg     120

gagccggtcc aggcggtgta cgggtttgcc aagagccttt tgaaggcgct aagagaagac     180

ggggacgcgg tgatcgtggt ctttgacgcc gaggccccct ccttccgcca cgaggcctac     240

ggggggtaca aggcggggcg ggctcccacc cccgaggact tccccggca gcttgccctt     300

atcaaggagc tggtggacct cctggggttt acccgcctcg aggtccccgg ctacgaggcg     360

gacgacgttc tcgccaccct ggccaagaag gcggaaaagg aggggtacga ggtgcgcatc     420

ctcaccgccg acaaagacct ttaccagctc ctttccgacc gcatccacgt cctccacccc     480

gaggggtacc tcatcacccc ggcctggctt tgggaaaagt acggcctgag ccccgaccag     540

tgggccgact accgggccct gaccggggac gagtccgaca accttcccgg ggtcaagggc     600
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- 2043 -

```
atcggggaga agaccgccct caagctcctc aaggagtggg ggagcctgga agccctcctc    660

aagaacctgg accggctgaa gcccgccatc cgggagaaga tcctggccca catggacgat    720

ctgaagctct cctgggacct ggccaaggtg cgcaccgacc tgcccctgga ggtggacttc    780

gccaaaaggc gggagcccga ccgggagggg cttaaggcct ttttggagag ctggagttc    840

ggcagcctcc tccacgagtt cggcctcctg ggaggggaga agccccggga ggaggccccc    900

tggcccccgc cggaaggggc cttcgtgggc tttgtgcttt cccgcaagga gcccatgtgg    960

gccgatcttc tggccctggc cgcctgcagg ggcggccgcg tgcaccgggc agcagacccc   1020

ttggcggggc taaaggacct caaggaggtc cggggcctcc tcgccaagga cctcgccgtc   1080

ttggcctcga gggagggggct agacctcgtg cccggggacg accccatgct cctcgcctac   1140

ctcctgggcc cctcgaacac caccccgag ggggtggcgc ggcgctacgg gggggagtgg   1200

acggaggacg ccgcccaccg ggccctcctc tcggagaggc tccatcggaa cctccttaag   1260

cgcctcgagg gggaggagaa gctcctttgg ctctaccacg aggtggaaaa gcccctctcc   1320

cgggtcctgg cccatatgga ggccaccggg gtacggctgg acgtggccta ccttcaggcc   1380

ctttccctgg agcttgcgga ggagatccgc cgcctcgagg aggaggtctt ccgcttggcg   1440

ggccacccct tcaacctcaa ctcccgggac cagctggaaa gggtgctctt tgacgagctt   1500

aggcttcccg ccttgaagaa gacgaagaag acaggcaagc gctccaccag cgccgcggtg   1560

ctggaggccc tacgggaggc ccaccccatc gtggagaaga tcctccagca ccgggagctc   1620

accaagctca agaacaccta cgtggacccc ctcccaagcc tcgtccaccc gaggacgggc   1680

cgcctccaca cccgcttcaa ccagacggcc acggccacgg ggaggcttag tagctccgac   1740

cccaacctgc agaacatccc cgtccgcacc cccttgggcc agaggatccg ccgggccttc   1800

gtggccgagg cgggttgggc gttggtggcc ctggactata gccagataga gctccgcgtc   1860

ctcgcccacc tctccgggga cgaaaacctg atcagggtct tccaggaggg gaaggacatc   1920

cacacccaga ccgcaagctg gatgttcggc gtcccccccgg aggccgtgga ccccctgatg   1980

cgccgggcgg ccaagacggt gaacttcggc gtcctctacg gcatgtccgc ccataggctc   2040

tcccaggagc ttgccatccc ctacgaggag gcggtggcct ttatagagcg ctacttccaa   2100

agcttcccca aggtgcgggc ctggatagaa aagaccctgg aggaggggag gaagcggggc   2160

tacgtggaaa ccctcttcgg aagaaggcgc tacgtgcccg acctcaacgc ccgggtgaag   2220

agcgtcaggg aggccgcgga gcgcatggcc ttcaacatgc ccgtccaggg caccgccgcc   2280

gacctcatga agctcgccat ggtgaagctc ttccccccgcc tccgggagat ggggggcccgc   2340

atgctcctcc aggtcgccaa cgagctcctc ctggaggccc cccaagcgcg ggccgaggag   2400

gtggcggctt tggccaagga ggccatggag aaggcctatc ccctcgccgt gcccctggag   2460
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- 2044 -

gtggaggtgg ggatggggga ggactggctt tccgccaagg gtcaccacca ccaccaccac   2520

<210> 2831

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2831

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1   5   10   15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
            20   25   30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
        35   40   45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Ala Val
    50   55   60

Ile Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr
65   70   75   80

Gly Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg
                85   90   95

Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg
            100   105   110

Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala
        115   120   125

Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp
    130   135   140

Lys Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro
145   150·   155   160

Glu Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu
                165   170   175

- 2045 -

Arg Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser
        180   185   190

Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys
        195   200   205

Leu Leu Lys Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp
        210   215   220

Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp
225   230   235   240

Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu
                245   250   255

Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys
                260   265   270

Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
        275   280   285

Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro Pro Pro
        290   295   300

Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp
305   310   315   320

Ala Asp Leu Leu Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg
                325   330   335

Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly
                340   345   350

Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp
        355   360   365

Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Gly Pro
        370   375   380

Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp
385   390   395   400

Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg
                405   410   415

Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr
                420   425   430

- 2046 -

His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
        435   440   445

Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu
        450   455   460

Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala
465   470   475   480

Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
                485   490   495

Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly
                500   505   510

Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His
        515   520   525

Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys
        530   535   540

Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly
545   550   555   560

Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
                565   570   575

Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu
                580   585   590

Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu
        595   600   605

Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
        610   615   620

Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile
625   630   635   640

His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val
                645   650   655

Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
                660   665   670

Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr

Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
    690   695   700

Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly
705   710   715   720

Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn
                725   730   735

Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
                740   745   750

Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val
        755   760   765

Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln
    770   775   780

Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu
785   790   795   800

Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala
                805   810   815

Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala
        820   825   830

Lys Gly His His His His His His
        835   840

<210>   2832

<211>   2526

<212>   DNA

<213>   Artificial Sequence

<220>

<223>   Synthetic

<400>   2832
atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtgcttct ggtggacggc   60

caccacctgg cctaccgcac cttcttcgcc ctgaagggcc tcaccaccag ccgcggggag   120

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ccggtgcaga tggtctacgg cttcgcccgg agcctcctca aggccttgaa ggaggacgga      180

caggcggtgg tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacgag      240

gcctacaagg cgggccgggc ccccaccccg gaggacttcc cccggcagct cgcccttatc      300

aaggagatgg tggacctttt gggcctggcg cgcctcgagg tcccgggcta cgaggcggac      360

gacgttctcg ccaccctggc caagaaggcg gaaaaggagg ggtacgaggt gcgcatcctc      420

accgccgacc gcgacctcta ccaactcgtc tccgaccgcg tcgccgtcct ccaccccgag      480

ggccacctca tcaccccgga gtggctttgg gagaagtacg gcctcaggcc ggagcagtgg      540

gtggacttcc gcgccctcgt gggggacccc tccgacaacc tccccggggt caagggcatc      600

ggggagaaga cggcggccaa gctgatccgg gagtggggaa gcctggaaaa ccttcttaag      660

cacctggaac aggtgaaacc tgcctccgtg cgggagaaga tccttagcca catggaggac      720

ctcaagctat ccctggagct atcccggggtg cacacggact tgctccttca ggtggacttt      780

aaggccctgc gccgcaggac ccccgacctg gagggcctga ggcctttttt ggaggagctg      840

gagttcggca gcctcctcca cgagttcggc ctcctggagg cccccgccgc ggcggaggaa      900

gctccctggc cgccccccga gggagccttc gtggggtacg ttctttcccg ccccgagccc      960

atgtgggcgg agcttaacgc cttggccgcc gcctggggcg gccgcgtgca ccgggcagca     1020

gacccccttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc     1080

gccgtcttgg cctcgaggga ggggctagac ctcgtgcccg gggacgaccc catgctcctc     1140

gcctacctcc tgggcccctc caacaccacc cccgaggggg tggcgcggcg ctacggggggg     1200

gagtggacgg aggacgccgc ccaccgggcc ctcctctcgg agaggctcca tcggaacctc     1260

cttaagcgcc tcgaggggga ggagaagctc ctttggctct accacgaggt ggaaaagccc     1320

ctctcccggg tcctggccca catggaggcc accggggtac ggctggacgt ggcctacctt     1380

caggcccttt ccctggagct tgcggaggag atccgccgcc tcgaggagga ggtcttccgc     1440

ttggcgggcc accccttcaa cctcaactcc cgggaccagc tggaaagggt gctctttgac     1500

gagcttaggc ttcccgcctt gaagaagacg aagaagacag gcaagcgctc caccagcgcc     1560

gcggtgctgg aggccctacg ggaggcccac cccatcgtgg agaagatcct ccagcaccgg     1620

gagctcacca agctcaagaa cacctacgtg gacccctcc caagcctcgt ccacccgagg     1680

acgggccgcc tccacacccg cttcaaccag acggccacgg ccacggggag gcttagtagc     1740

tccgacccca acctgcagaa catcccccgtc cgcacccct tgggccagag gatccgccgg     1800

gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc     1860

cgcgtcctcg cccacctctc cggggacgaa aacctgatca gggtcttcca ggagggggaag     1920

gacatccaca cccagaccgc aagctggatg ttcggcgtcc ccccggaggc cgtggacccc     1980
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- 2049 -

```
ctgatgcgcc gggcggccaa gacggtgaac ttcggcgtcc tctacggcat gtccgcccat    2040

aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac    2100

ttccaaagct tccccaaggt gcgggcctgg atagaaaaga ccctggagga ggggaggaag    2160

cggggctacg tggaaaccct cttcggaaga aggcgctacg tgcccgacct caacgcccgg    2220

gtgaagagcg tcagggaggc cgcggagcgc atggccttca acatgcccgt ccagggcacc    2280

gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg    2340

gcccgcatgc tcctccaggt cgccaacgag ctcctcctgg aggcccccca agcgcgggcc    2400

gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc    2460

ctggaggtgg aggtggggat ggggggaggac tggctttccg ccaagggtca ccaccaccac    2520

caccac                                                                2526
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<210> 2833

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2833

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Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1               5                   10                  15


Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys
            20                  25                  30


Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Met Val Tyr Gly Phe
        35                  40                  45


Ala Arg Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Gln Ala Val Val
    50                  55                  60


Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu
65                  70                  75                  80


Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
                85                  90                  95


Leu Ala Leu Ile Lys Glu Met Val Asp Leu Leu Gly Leu Ala Arg Leu
```

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                100                    105                    110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys
        115                 120                 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg
        130                 135                 140

Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His Pro Glu
145                 150                 155                 160

Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Arg
                165                 170                 175

Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro Ser Asp
                180                 185                 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala Lys Leu
        195                 200                 205

Ile Arg Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys His Leu Glu Gln
        210                 215                 220

Val Lys Pro Ala Ser Val Arg Glu Lys Ile Leu Ser His Met Glu Asp
225                 230                 235                 240

Leu Lys Leu Ser Leu Glu Leu Ser Arg Val His Thr Asp Leu Leu Leu
                245                 250                 255

Gln Val Asp Phe Lys Ala Leu Arg Arg Arg Thr Pro Asp Leu Glu Gly
                260                 265                 270

Leu Arg Ala Phe Leu Glu Glu Leu Glu Phe Gly Ser Leu Leu His Glu
        275                 280                 285

Phe Gly Leu Leu Glu Ala Pro Ala Ala Ala Glu Glu Ala Pro Trp Pro
        290                 295                 300

Pro Pro Glu Gly Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro
305                 310                 315                 320

Met Trp Ala Glu Leu Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val
                325                 330                 335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
        340                 345                 350
```

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
        355   360   365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
        370   375   380

Gly Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
385   390   395   400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
            405   410   415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
        420   425   430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
        435   440   445

Glu Ala Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser
    450   455   460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
465   470   475   480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
            485   490   495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
        500   505   510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
        515   520   525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
    530.   535   540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
545   550   555   560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
            565   570   575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
        580   585   590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
        595   600   605

```
Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
    610                 615                 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
625                 630                 635                 640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
                645                 650                 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
                660                 665                 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
        675                 680                 685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
        690                 695                 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
705                 710                 715                 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
                725                 730                 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
                740                 745                 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
        755                 760                 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
    770                 775                 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
785                 790                 795                 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
                805                 810                 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
                820                 825                 830

Ser Ala Lys Gly His His His His His
        835                 840
```

<210> 2834

<211> 2511

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2834

```
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ctggcctacc gcaccttcca cgccctgaag ggcctcacca ccagccgcgg ggagccggtc  120

caggcggtgt acgggtttgc caagagcctt ttgaaggcgc taagagaaga cggggatgtg  180

gtgatcgtgg tctttgacgc caaggccccc tccttccgcc acgaggccta cgggggggtac  240

aaggcgggcc gggccccgac ccccgaggac ttcccccggc agctcgccct catcaaggag  300

ctggtggacc tcctggggct ggcgcgcctc gaggtgccgg gctttgaagc ggatgacgtc  360

ctggctaccc tggccaagaa ggcggaaaag gagggctacg aggtgcgcat tctcaccggc  420

gaccgcgacc tttaccaact cgtctccgac cgcgtcgccg tcctccaccc cgagggccac  480

ctcatcaccc cggagtggct ttgggagaag tacggcctca ggccggagca gtgggtggac  540

taccgggcct tggccgggga cccttccgac aacatccccg gcgtgaaggg catcggggag  600

aagacggcga ggaagcttct ggaggagtgg gggagcgtgg aagccctcct caagaacctg  660

gaccggctga gcccgccat ccgggagaag atcctggccc acatggagga cctcaagcta  720

tccctggagc tatcccgggt gcgcaccgac ctccccctgg aggtggacct cgcccagggg  780

cgggagcccg accgggaggg gcttaaggcc tttttggaga ggctggagtt cggaagcctc  840

ctccacgagt tcggcctgtt ggaaagcccg gtggcggcgg aggaagctcc ctggccgccc  900

cccgagggag ccttcgtggg gtacgttctt tcccgccccg agcccatgtg ggcggagctt  960

aacgccttgg ccgccgcctg gggcggccgc gtgcaccggg cagcagaccc cttggcgggg 1020

ctaaaggacc tcaaggaggt ccggggcctc ctcgccaagg acctcgccgt cttggcctcg 1080

agggaggggc tagacctcgt gcccgggggac gaccccatgc tcctcgccta cctcctgggc 1140

ccctccaaca ccacccccga ggggtggcg cggcgctacg ggggggagtg gacggaggac 1200

gccgcccacc gggccctcct ctcggagagg ctccatcgga acctccttaa gcgcctcgag 1260

ggggaggaga agctcctttg gctctaccac gaggtggaaa agcccctctc ccgggtcctg 1320

gcccacatgg aggccaccgg ggtacggctg acgtggcct accttcaggc cctttccctg 1380

gagcttgcgg aggagatccg ccgcctcgag gaggaggtct ccgcttggc gggccacccc 1440

ttcaacctca actcccggga ccagctggaa aggtgctct ttgacgagct taggcttccc 1500
```

```
gccttgaaga agacgaagaa gacaggcaag cgctccacca gcgccgcggt gctggaggcc     1560

ctacgggagg cccacccat cgtggagaag atcctccagc accgggagct caccaagctc     1620

aagaacacct acgtggaccc cctcccaagc ctcgtccacc cgaggacggg ccgcctccac     1680

acccgcttca accagacggc cacggccacg gggaggctta gtagctccga ccccaacctg     1740

cagaacatcc ccgtccgcac ccccttgggc cagaggatcc gccgggcctt cgtggccgag     1800

gcgggttggg cgttggtggc cctggactat agccagatag agctccgcgt cctcgcccac     1860

ctctccgggg acgaaaacct gatcagggtc ttccaggagg ggaaggacat ccacacccag     1920

accgcaagct ggatgttcgg cgtccccccg gaggccgtgg accccctgat gcgccgggcg     1980

gccaagacgg tgaacttcgg cgtcctctac ggcatgtccg cccataggct ctcccaggag     2040

cttgccatcc cctacgagga ggcggtggcc tttatagagc gctacttcca aagcttcccc     2100

aaggtgcggg cctggataga aaagaccctg gaggagggga ggaagcgggg ctacgtggaa     2160

accctcttcg gaagaaggcg ctacgtgccc gacctcaacg cccgggtgaa gagcgtcagg     2220

gaggccgcgg agcgcatggc cttcaacatg cccgtccagg gcaccgccgc cgacctcatg     2280

aagctcgcca tggtgaagct cttcccccgc ctccgggaga tggggggccg catgctcctc     2340

caggtcgcca acgagctcct cctggaggcc ccccaagcgc gggccgagga ggtggcggct     2400

ttggccaagg aggccatgga gaaggcctat cccctcgccg tgcccctgga ggtggaggtg     2460

gggatggggg aggactggct ttccgccaag ggtcaccacc accaccacca c             2511
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<210>   2835

<211>   837

<212>   PRT

<213>   Artificial Sequence

<220>

<223>   Synthetic

<400>   2835

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Met Glu Phe Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val
1               5                   10                  15


Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly Leu
            20                  25                  30


Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
        35                  40                  45
```

Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val
    50   55   60

Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly Tyr
65   70   75   80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
                85   90   95

Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu Val
            100   105   110

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
            115   120   125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Gly Asp Arg Asp Leu
    130   135   140

Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His Pro Glu Gly His
145   150   155   160

Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Glu
                165   170   175

Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile
            180   185   190

Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu
            195   200   205

Glu Trp Gly Ser Val Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys
    210   215   220

Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Glu Asp Leu Lys Leu
225   230   235   240

Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu Pro Leu Glu Val Asp
            245   250   255

Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala Phe Leu
            260   265   270

Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu
            275   280   285

Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala
    290   295   300

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```
Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu Leu
305             310             315             320

Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val His Arg Ala Ala Asp
            325             330             335

Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu Ala
            340             345             350

Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val Pro
        355             360             365

Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Gly Pro Ser Asn Thr
    370             375             380

Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp
385             390             395             400

Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu Leu
            405             410             415

Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu Val
        420             425             430

Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly Val
        435             440             445

Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu
    450             455             460

Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His Pro
465             470             475             480

Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu
            485             490             495

Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser
        500             505             510

Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val
        515             520             525

Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr
    530             535             540

Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu His
```

```
545                     550                     555                     560

Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser
            565                 570                 575

Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg
            580                 585                 590

Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala Leu
            595                 600                 605

Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp
        610                 615                 620

Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr Gln
625                 630                 635                 640

Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro Leu
            645                 650                 655

Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly Met
            660                 665                 670

Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala
        675                 680                 685

Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala
        690                 695                 700

Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu
705                 710                 715                 720

Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg Val
            725                 730                 735

Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val
            740                 745                 750

Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe
        755                 760                 765

Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala Asn
        770                 775                 780

Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala Ala
785                 790                 795                 800
```

Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu
                805   .   810   815

Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys Gly His
                820   825   830

His His His His His
         835

<210> 2836

<211> 2493

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2836

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ctggcctacc gtaccttttt tgccctgaag ggcctcacca cctcccgggg ggagccggtg   120

cagatggtct acggcttcgc ccggagcctc ctcaaggccc tcaaggagga cggggacgcg   180

gtgatcgtgg tctttgacgc cgaggccccc tccttccgcc accagaccta cgaggcctac   240

aaggcgggga gggctcccac ccccgaggac tttccccggc agcttgccct tatcaaggag   300

ctggtggacc tcctggggtt tacccgcctc gaggtccccg ctacgaggc ggacgacgtt   360

ctcgccaccc tggccaagaa ggcggaaaag gagggctacg aggtgcgcat cctcaccgcg   420

gaccgggacc tttaccagct tctttccgac cgcattcacg tccttcaccc cgagggggtac   480

ctcatcaccc cggcctggct ttgggaaaag tacggcttga ggcccgacca gtgggccgac   540

taccgggccc tgaccgggga cgaatccgac aacctttccg gggtcaaggg catcggggag   600

aagacggcga ggaagcttct ggaggagtgg gggagcctgg aagccctcct caagaacctg   660

gaccggctga gcccgccat ccgggagaag atcctggccc acatggacga tctgaagctc   720

tccttggagc tctcccgggt gcgcaccgac ctccccctgg aggtggactt cgccaaaagg   780

cgggagcccg accgggagag gcttagggcc tttctggaga ggcttgagtt tggcagcctc   840

ctccacgagt tcggcccttt ggaaagcccc agggccgcgg aggaagctcc ctggccgccc   900

cccgagggag ccttcgtggg gtacgttctt tcccgccccg agcccatgtg ggcggagctt   960

aacgccttgg ccgccgccag gggcggccgc gtgcaccggg cagcagaccc cttggcgggg  1020

ctaaaggacc tcaaggaggt ccggggcctc ctcgccaagg acctcgccgt cttggcctcg  1080
```

```
agggaggggc tagacctcgt gcccggggac gaccccatgc tcctcgccta cctcctgggc    1140

ccctcgaaca ccaccccccga ggggggtggcg cggcgctacg ggggggagtg gacggaggac    1200

gccgcccacc gggccctcct ctcggagagg ctccatcgga acctccttaa gcgcctcgag    1260

ggggaggaga agctcctttg gctctaccac gaggtggaaa agcccctctc ccgggtcctg    1320

gcccatatgg aggccaccgg ggtacggctg gacgtggcct accttcaggc cctttccctg    1380

gagcttgcgg aggagatccg ccgcctcgag gaggaggtct tccgcttggc gggccacccc    1440

ttcaacctca actcccggga ccagctggaa agggtgctct ttgacgagct taggcttccc    1500

gccttgaaga agacgaagaa gacaggcaag cgctccacca gcgccgcggt gctggaggcc    1560

ctacgggagg cccaccccat cgtggagaag atcctccagc accgggagct caccaagctc    1620

aagaacacct acgtggaccc cctcccaagc ctcgtccacc cgaggacggg ccgcctccac    1680

acccgcttca accagacggc cacggccacg gggaggctta gtagctccga ccccaacctg    1740

cagaacatcc ccgtccgcac ccccttgggc cagaggatcc gccgggcctt cgtggccgag    1800

gcgggttggg cgttggtggc cctggactat agccagatag agctccgcgt cctcgcccac    1860

ctctccgggg acgaaaacct gatcagggtc ttccaggagg ggaaggacat ccacacccag    1920

accgcaagct ggatgttcgg cgtccccccg gaggccgtgg accccctgat gcgccgggcg    1980

gccaagacgg tgaacttcgg cgtcctctac ggcatgtccg cccataggct ctcccaggag    2040

cttgccatcc cctacgagga ggcggtggcc tttatagagc gctacttcca aagcttcccc    2100

aaggtgcggg cctggataga aaagaccctg gaggagggga ggaagcgggg ctacgtggaa    2160

accctcttcg gaagaaggcg ctacgtgccc gacctcaacg cccgggtgaa gagcgtcagg    2220

gaggccgcgg agcgcatggc cttcaacatg cccgtccagg gcaccgccgc cgacctcatg    2280

aagctcgcca tggtgaagct cttcccccgc ctccgggaga tggggggcccg catgctcctc    2340

caggtcgcca acgagctcct cctggaggcc ccccaagcgc gggccgagga ggtggcggct    2400

ttggccaagg aggccatgga gaaggcctat cccctcgccg tgcccctgga ggtggaggtg    2460

gggatggggg aggactggct ttccgccaag ggt                               2493
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<210> 2837

<211> 831

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2837

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Met Asn Ser Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val
1               5               10              15

Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu
        20              25              30

Thr Thr Ser Arg Gly Glu Pro Val Gln Met Val Tyr Gly Phe Ala Arg
        35              40              45

Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val Val
    50              55              60

Phe Asp Ala Glu Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr
65              70              75              80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
            85              90              95

Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu Glu Val
            100             105             110

Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
            115             120             125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu
    130             135             140

Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr
145             150             155             160

Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp
            165             170             175

Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu
            180             185             190

Ser Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu
            195             200             205

Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys
            210             215             220

Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu
225             230             235             240
```

Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu Pro Leu Glu Val Asp
                245   250   255

Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe Leu
                260   265   270

Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Pro Leu Glu
                275   280   285

Ser Pro Arg Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala
        290   295   300

Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu Leu
305   310   315   320

Asn Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala Ala Asp
                325   330   335

Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu Ala
            340   345   350

Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val Pro
        355   360   365

Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Gly Pro Ser Asn Thr
    370   375   380

Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp
385   390   395   400

Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu Leu
                405   410   415

Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu Val
            420   425   430

Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly Val
        435   440   445

Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu
        450   455   460

Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His Pro
465   470   475   480

Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu
                485   490   495

```
Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser
         500              505              510

Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val
         515              520              525

Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr
         530              535              540

Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu His
545              550              555              560

Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser
             565              570              575

Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg
             580              585              590

Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala Leu
         595              600              605

Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp
         610              615              620

Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr Gln
625              630              635              640

Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro Leu
             645              650              655

Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly Met
             660              665              670

Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala
         675              680              685

Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala
         690              695              700

Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu
705              710              715              720

Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg Val
             725              730              735

Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val
```

```
                  740                     745                     750

         Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe
                 755                 760                 765


         Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala Asn
                 770                 775                 780


         Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala Ala
         785                 790                 795                 800


         Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu
                     805                 810                 815


         Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys Gly
                 820                 825                 830
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<210> 2838

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2838

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ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc       120

gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac       180

gggtacaagg ccgtcttcgt ggtctttgac gccaaggccc cctccttccg ccacgaggcc       240

tacgaggcct acaaggcggg gagggccccg accccgagg acttcccccg gcagctcgcc        300

ctcatcaagg agctggtgga cctcctgggg tttacccgcc tcgaggtccc cggctacgag       360

gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc       420

atcctcaccg ccgaccgcga cctctaccaa ctcgtctccg accgcgtcgc cgtcctccac       480

cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag       540

cagtgggtgg acttccgcgc cctcgtgggg gacccctccg acaacctccc cggggtcaag       600

ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc       660

ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg       720
```

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gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggaggtg    780

gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg    840

gagttcggca gcctcctcca cgagttcggc ctcctggagg cccccgcccc cctggaggag    900

gcccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccg ccccgagccc    960

atgtgggcgg agcttaaagc cctggccgcc tgcaggggcg gccgcgtgca ccgggcagca   1020

gaccccttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc   1080

gccgtcttgg cctcgaggga ggggctagac ctcgtgcccg gggacgaccc catgctcctc   1140

gcctacctcc tggacccttc gaacaccacc cccgaggggg tggcgcggcg ctacgggggg   1200

gagtggacgg aggacgccgc ccaccgggcc ctcctctcgg agaggctcca tcggaacctc   1260

cttaagcgcc tcgagggga ggagaagctc ctttggctct accacgaggt ggaaaagccc   1320

ctctcccggg tcctggccca catggaggcc accggggtac ggctggacgt ggcctacctt   1380

caggcccttt ccctggagct tgcggaggag atccgccgcc tcgaggagga ggtcttccgc   1440

ttggcgggcc accccttcaa cctcaactcc cgggaccagc tggaaagggt gctctttgac   1500

gagcttaggc ttccccgcctt gaagaagacg aagaagacag gcaagcgctc caccagcgcc   1560

gcggtgctgg aggccctacg ggaggcccac cccatcgtgg agaagatcct ccagcaccgg   1620

gagctcacca agctcaagaa cacctacgtg gacccctcc caagcctcgt ccacccgagg   1680

acgggccgcc tccacacccg cttcaaccag acggccacgg ccacggggag gcttagtagc   1740

tccgacccca acctgcagaa catccccgtc cgcacccccт tgggccagag gatccgccgg   1800

gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc   1860

cgcgtcctcg cccacctctc cggggacgaa aacctgatca gggtcttcca ggaggggaag   1920

gacatccaca cccagaccgc aagctggatg ttcggcgtcc ccccggaggc cgtggacccc   1980

ctgatgcgcc gggcggccaa gacggtgaac ttcggcgtcc tctacggcat gtccgcccat   2040

aggctctccc aggagcttgc catccccтac gaggaggcgg tggcctttat agagcgctac  2100

ttccaaagct tccccaaggt gcgggcctgg atagaaaaga ccctggagga ggggaggaag   2160

cggggctacg tggaaaccct cttcggaaga aggcgctacg tgcccgacct caacgcccgg   2220

gtgaagagcg tcagggaggc cgcggagcgc atggccttca acatgcccgt ccagggcacc   2280

gccgccgacc tcatgaagct cgccatggtg aagctcttcc ccgcctccg ggagatgggg   2340

gcccgcatgc tcctccaggt cgccaacgag ctcctcctgg aggccccca agcgcgggcc   2400

gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc   2460

ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggtca ccaccaccac   2520

caccac                                                             2526
```

<210> 2839

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2839

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1   5   10   15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
                20   25   30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
            35   40   45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
        50   55   60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
65   70   75   80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
                85   90   95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
                100   105   110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
            115   120   125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
        130   135   140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
145   150   155   160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
                165   170   175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
            180   185   190

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```
Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
        195             200             205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
        210             215             220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
225             230             235             240

Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
                245             250             255

Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
            260             265             270

Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
        275             280             285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
    290             295             300

Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
305             310             315             320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
            325             330             335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
        340             345             350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
        355             360             365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
    370             375             380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
385             390             395             400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
            405             410             415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
        420             425             430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
```

```
                435                     440                     445

Glu Ala Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser
    450                 455                 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Val Phe Arg
465                 470                 475                 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
                485                 490                 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
                500                 505                 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
            515                 520                 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
    530                 535                 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
545                 550                 555                 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
                565                 570                 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
            580                 585                 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
        595                 600                 605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
    610                 615                 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
625                 630                 635                 640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
                645                 650 .               655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
            660                 665                 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
        675                 680                 685

                            - 2068 -
```

```
Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
    690               695               700
```

```
Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
705               710               715               720
```

```
Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
            725               730               735
```

```
Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
            740               745               750
```

```
Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
        755               760               765
```

```
Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
    770               775               780
```

```
Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
785               790               795               800
```

```
Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
            805               810               815
```

```
Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
            820               825               830
```

```
Ser Ala Lys Gly His His His His His His
            835               840
```

<210> 2840

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2840
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ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc   120

gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac   180

gggtacaagg ccgtcttcgt ggtctttgac gccaaggccc cctccttccg ccacgaggcc   240

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```

```
tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc      300

ctcatcaagg agctggtgga cctcctgggg tttacccgcc tcgaggtccc cggctacgag      360

gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc      420

atcctcaccg ccgaccgcga cctctaccaa ctcgtctccg accgcgtcgc cgtcctccac      480

cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag      540

cagtgggtgg acttccgcgc cctcgtgggg gaccccctccg acaacctccc cggggtcaag      600

ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc      660

ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg      720

gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggaggtg      780

gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg      840

gagttcggca gcctcctcca cgagttcggc ctcctggagg cccccgcccc cctggaggag      900

gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccg ccccgagccc      960

atgtgggcgg agcttaaagc cctggccgcc tgcaggggcg gccgcgtgca ccgggcagca     1020

gacccccttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc     1080

gccgtcttgg cctcgaggga ggggctagac ctcgtgcccg gggacgaccc catgctcctc     1140

gcctacctcc tgggcccctc caacaccacc cccgaggggg tggcgcggcg ctacggggg g     1200

gagtggacgg aggacgccgc ccaccgggcc ctcctctcgg agaggctcca tcggaacctc     1260

cttaagcgcc tcgaggggga ggagaagctc ctttggctct accacgaggt ggaaaagccc     1320

ctctcccggg tcctggccca catggaggcc accggggtac ggcgggacgt ggcctacctt     1380

caggcccttt ccctggagct tgcggaggag atccgccgcc tcgaggagga ggtcttccgc     1440

ttggcgggcc accccttcaa cctcaactcc cgggaccagc tggaaagggt gctctttgac     1500

gagcttaggc ttcccgcctt gaagaagacg aagaagacag gcaagcgctc caccagcgcc     1560

gcggtgctgg aggccctacg ggaggcccac cccatcgtgg agaagatcct ccagcaccgg     1620

gagctcacca agctcaagaa cacctacgtg accccctcc caagcctcgt ccacccgagg     1680

acgggccgcc tccacacccg cttcaaccag acggccacgg ccacggggag gcttagtagc     1740

tccgacccca acctgcagaa catccccgtc cgcaccccct ggggccagag gatccgccgg     1800

gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc     1860

cgcgtcctcg cccacctctc cgggggacgaa aacctgatca gggtcttcca ggaggggaag     1920

gacatccaca cccagaccgc aagctggatg ttcggcgtcc ccccggaggc cgtggacccc     1980

ctgatgcgcc gggcggccaa gacggtgaac ttcggcgtcc tctacggcat gtccgcccat     2040

aggctctccc aggagcttgc catccccタック gaggaggcgg tggcctttat agagcgctac     2100
```

```
ttccaaagct tccccaaggt gcgggcctgg atagaaaaga ccctggagga ggggaggaag    2160

cggggctacg tggaaaccct cttcggaaga aggcgctacg tgcccgacct caacgcccgg    2220

gtgaagagcg tcagggaggc cgcggagcgc atggccttca acatgcccgt ccagggcacc    2280

gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg    2340

gcccgcatgc tcctccaggt cgccaacgag ctcctcctgg aggccccccca agcgcgggcc    2400

gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc    2460

ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggtca ccaccaccac    2520

caccac                                                              2526
```

<210> 2841

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2841

```
Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1               5                   10                  15


Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
            20                  25                  30


Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
        35                  40                  45


Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
    50                  55                  60


Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
65                  70                  75                  80


Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
                85                  90                  95


Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
            100                 105                 110


Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
```

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Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
    130   135   140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
145   150   155   160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
                165   170   175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
            180   185   190

Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
                195   200   205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
    210   215   220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
225   230   235   240

Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
            245   250   255

Pro Leu Glu Val Asp Leu Ala Gln. Gly Arg Glu Pro Asp Arg Glu Gly
            260   265   270

Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
            275   280   285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
    290   295   300

Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
305   310   315   320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
                325   330   335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
            340   345   350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
    355   360   365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
    370   375   380

Gly Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
385   390   395   400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
            405   410   415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
            420   425   430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
        435   440   445

Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
    450   455   460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
465   470   475   480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
            485   490   495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
            500   505   510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
        515   520   525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
    530   535   540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
545   550   555   560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
        565   570   575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
        580   585   590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
        595   600   605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
    610   615   620

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```
His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
625             630             635                 640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
                645             650                 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
            660             665                 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
        675             680             685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
    690             695             700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
705             710             715                 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
            725             730             735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
            740             745             750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
        755             760             765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
    770             775             780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
785             790             795                 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
            805             810             815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
            820             825             830

Ser Ala Lys Gly His His His His His His
        835             840
```

<210> 2842

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2842
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ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc   120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac   180
gggtacaagg ccgtcttcgt ggtctttgac gccaaggccc cctccttccg ccacgaggcc   240
tacgaggcct acaaggcggg gagggccccg accccgagg  acttcccccg gcagctcgcc   300
ctcatcaagg agctggtgga cctcctgggg tttacccgcc tcgaggtccc cggctacgag   360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc   420
atcctcaccg ccgaccgcga cctctaccaa ctcgtctccg accgcgtcgc cgtcctccac   480
cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag   540
cagtgggtgg acttccgcgc cctcgtgggg gacccctccg acaacctccc cggggtcaag   600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc   660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg   720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggaggtg   780
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg   840
gagttcggca gcctcctcca cgagttcggc ctcctggagg cccccgcccc cctggaggag   900
gcccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccg ccccgagccc   960
atgtgggcgg agcttaaagc cctggccgcc tgcaggggcg gccgcgtgca ccgggcagca  1020
gaccccttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc  1080
gccgtcttgg cctcgaggga ggggctagac ctcgtgcccg gggacgaccc catgctcctc  1140
gcctacctcc tggacccttc gaacaccacc cccgaggggg tggcgcggcg ctacgggggg  1200
gagtggacgg aggacgccgc ccaccgggcc ctcctctcgg agaggctcca tcggaacctc  1260
cttaagcgcc tcgaggggga ggagaagctc ctttggctct accacgaggt ggaaaagccc  1320
ctctcccggg tcctggccca catggaggcc accgggggtac ggcgggacgt ggcctacctt  1380
caggcccttt ccctggagct tgcggaggag atccgccgcc tcgaggagga ggtcttccgc  1440
ttggcgggcc accccttcaa cctcaactcc cgggaccagc tggaaagggt gctctttgac  1500
gagcttaggc ttcccgcctt gaagaagacg aagaagacag caagcgctc  caccagcgcc  1560
gcggtgctgg aggccctacg ggaggcccac cccatcgtgg agaagatcct ccagcaccgg  1620
```

gagctcacca agctcaagaa cacctacgtg gaccccctcc caagcctcgt ccacccgagg   1680

acgggccgcc tccacacccg cttcaaccag acggccacgg ccacggggag gcttagtagc   1740

tccgacccca acctgcagaa catccccgtc cgcaccccct gggccagag gatccgccgg   1800

gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc   1860

cgcgtcctcg cccacctctc cggggacgaa aacctgatca gggtcttcca ggaggggaag   1920

gacatccaca cccagaccgc aagctggatg ttcggcgtcc ccccggaggc cgtggacccc   1980

ctgatgcgcc gggcggccaa gacggtgaac ttcggcgtcc tctacggcat gtccgcccat   2040

aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac   2100

ttccaaagct tccccaaggt gcgggcctgg atagaaaaga ccctggagga ggggaggaag   2160

cggggctacg tggaaaccct cttcggaaga aggcgctacg tgcccgacct caacgcccgg   2220

gtgaagagcg tcagggaggc cgcggagcgc atggccttca acatgcccgt ccagggcacc   2280

gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg   2340

gcccgcatgc tcctccaggt cgccaacgag ctcctcctgg aggccccca agcgcgggcc   2400

gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc   2460

ctggaggtgg aggtgggggat gggggaggac tggctttccg ccaagggtca ccaccaccac   2520

caccac   2526

<210> 2843

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2843

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1   5   10   15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
                20   25   30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
            35   40   45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala

```
                50                      55                      60

        Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
        65              70              75                      80


        Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
                        85              90                      95


        Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
                        100             105             110


        Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
                        115             120             125


        Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
                130             135             140


        Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
        145             150             155             160


        Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
                        165             170             175


        Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
                        180             185             190


        Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
                        195             200             205


        Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
                210             215             220


        Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
        225             230             235             240


        Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
                        245             250             255


        Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
                        260             265             270


        Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
                        275             280             285


        Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
                290             295             300


                                    - 2077 -
```

```
Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
305                 310             315             320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
                325             330             335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
                340             345             350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
            355             360             365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
    370             375             380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
385             390             395             400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
                405             410             415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
            420             425             430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
        435             440             445

Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
    450             455             460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
465             470             475             480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
                485             490             495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
            500             505             510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
            515             520             525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
    530             535             540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
545             550             555             560
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Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
                565   570   575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
            580   585   590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
            595   600   605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
        610   615   620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
625   630   635   640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
                645   650   655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
            660   665   670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
        675   680   685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
    690   695   700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
705   710   715   720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
            725   730   735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
            740   745   750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
        755   760   765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
        770   775   780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
785   790   795   800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
        820   825   830

Ser Ala Lys Gly His His His His His His
        835   840

<210> 2844

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2844
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gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac   180

gggtacaagg ccgtcttcgt ggtctttgac gccaaggccc cctccttccg ccacgaggcc   240

tacgaggcct acaaggcggg gagggccccg accccgagg acttcccccg gcagctcgcc   300

ctcatcaagg agctggtgga cctcctgggg tttacccgcc tcgaggtccc cggctacgag   360

gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc   420

atcctcaccg ccgaccgcga cctctaccaa ctcgtctccg accgcgtcgc cgtcctccac   480

cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag   540

cagtgggtgg acttccgcgc cctcgtgggg gacccctccg acaacctccc cggggtcaag   600

ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc   660

ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg   720

gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggaggtg   780

gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg   840

gagttcggca gcctcctcca cgagttcggc ctcctggagg cccccgcccc cctggaggag   900

gcccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccg ccccgagccc   960

atgtgggcgg agcttaaagc cctggccgcc tgcagggggcg ccgcgtgca ccgggcagca   1020

gaccccttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc   1080

- 2080 -

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gccgtcttgg cctcgaggga ggggctagac ctcgtgcccg gggacgaccc catgctcctc    1140

gcctacctcc tgggcccctc caacaccacc cccgaggggg tggcgcggcg ctacggggggg   1200

gagtggacgg aggacgccgc ccaccgggcc ctcctctcgg agaggctcca tcggaacctc    1260

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ctctcccggg tcctggccca catggaggcc accggggtac ggctggacgt ggcctacctt    1380

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gagcttaggc ttcccgcctt gaagaagacg aagaagacag gcaagcgctc caccagcgcc    1560

gcggtgctgg aggccctacg ggaggcccac cccatcgtgg agaagatcct ccagcaccgg    1620

gagctcacca agctcaagaa cacctacgtg accccctcc caagcctcgt ccacccgagg    1680

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cgcgtcctcg cccacctctc cggggacgaa aacctgatca gggtcttcca ggaggggaag    1920

gacatccaca cccagaccgc aagctggatg ttcggcgtcc ccccggaggc cgtggacccc    1980

ctgatgcgcc gggcggccaa gacggtgaac ttcggcgtcc tctacggcat gtccgcccat    2040

aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac    2100

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cggggctacg tggaaaccct cttcggaaga aggcgctacg tgcccgacct caacgcccgg    2220

gtgaagagcg tcagggaggc cgcggagcgc atggccttca acatgcccgt ccagggcacc    2280

gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg    2340

gcccgcatgc tcctccaggt cgccaacgag ctcctcctgg aggcccccca agcgcgggcc    2400

gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc    2460

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caccac                                                                2526


<210>  2845

<211>  842

<212>  PRT

<213>  Artificial Sequence


<220>
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<223> Synthetic

<400> 2845

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1   5   10   15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Arg Phe Ala Leu
            20   25   30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
            35   40   45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
    50   55   60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
65   70   75   80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
                85   90   95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
            100   105   110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
            115   120   125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
    130   135   140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
145   150   155   160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
            165   170   175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
            180   185   190

Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
    195   200   205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
    210   215   220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
225   230   235   240

Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
245   250   255

Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
        260   265   270

Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
        275   280   285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
    290   295   300

Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
305   310   315   320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
            325   330   335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
        340   345   350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
        355   360   365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
    370   375   380

Gly Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
385   390   395   400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
            405   410   415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
        420   425   430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
        435   440   445

Glu Ala Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser
    450   · 455   460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
465   470   475   480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
            500   505   510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
            515   520   525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
            530   535   540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
545   550   555   560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
                565   570   575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
            580   585   590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
            595   600   605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
            610   615   620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
625   630   635   640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
                645   650   655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
            660   665   670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
            675   680   685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
            690   695   700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
705   710   715   720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
                725   730   735

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Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
            740             745             750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
            755             760             765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
    770             775.            780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
785             790             795             800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
            805             810             815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
            820             825             830

Ser Ala Lys Gly His His His His His
        835             840
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<210> 2846

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2846
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gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac     180

gggtacaagg ccgtcttcgt ggtctttgac gccaaggccc cctccttccg ccacgaggcc     240

tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc     300

ctcatcaagg agctggtgga cctcctgggg tttacccgcc tcgaggtccc cggctacgag     360

gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc     420

atcctcaccg ccgaccgcga cctctaccaa ctcgtctccg accgcgtcgc cgtcctccac     480

cccgagggcc acctcatcac cccggagtgg ctttgggaga gtacggcct caggccggag     540

cagtgggtgg acttccgcgc cctcgtgggg gaccccctccg acaacctccc cggggtcaag     600
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ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc      660

ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg      720

gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggaggtg      780

gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg      840

gagttcggca gcctcctcca cgagttcggc ctcctggagg cccccgcccc cctggaggag      900

gcccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccg ccccgagccc      960

atgtgggcgg agcttaaagc cctggccgcc tgcaggggcg gccgcgtgca ccgggcagca     1020

gaccccttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc     1080

gccgtcttgg cctcgaggga ggggctagac ctcgtgcccg gggacgaccc catgctcctc     1140

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cttaagcgcc tcgaggggga ggagaagctc ctttggctct accacgaggt ggaaaagccc     1320

ctctcccggg tcctggccca catggaggcc accggggtac ggctggacgt ggcctacctt     1380

caggcccttt ccctggagct tgcggaggag atccgccgcc tcgaggagga ggtcttccgc     1440

ttggcgggcc accccttcaa cctcaactcc cgggaccagc tggaaagggt gctctttgac     1500

gagcttaggc ttcccgcctt gaagaagacg aagaagacag gcaagcgctc caccagcgcc     1560

gcggtgctgg aggccctacg ggaggcccac cccatcgtgg agaagatcct ccagcaccgg     1620

gagctcacca agctcaagaa cacctacgtg gaccccctcc caagcctcgt ccacccgagg     1680

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gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc     1860

cgcgtcctcg cccacctctc cggggacgaa aacctgatca gggtcttcca ggaggggaag     1920

gacatccaca cccagaccgc aagctggatg ttcggcgtcc ccccggaggc cgtggacccc     1980

ctgatgcgcc gggcggccaa gaccggtgaac ttcggcgtcc tctacggcat gtccgcccat     2040

aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac     2100

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cggggctacg tggaaaccct cttcggaaga aggcgctacg tgcccgacct caacgcccgg     2220

gtgaagagcg tcagggaggc cgcggagcgc atggccttca acatgcccgt ccagggcacc     2280

gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg     2340

gcccgcatgc tcctccaggt cgccaacgag ctcctcctgg aggccccca agcgcgggcc     2400

gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc     2460
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caccac   2526

<210>   2847

<211>   842

<212>   PRT

<213>   Artificial Sequence

<220>

<223>   Synthetic

<400>   2847

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1   5   10   15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Arg His Ala Leu
                20   25   30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
            35   40   45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
    50   55   60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
65   70   75   80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
                85   90   95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
                100   105   110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
                115   120   125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
            130   135   140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
145   150   155   160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly

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Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
            180   185   190

Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
            195   200   205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
    210   215   220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
225   230   235   240

Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
            245   250   255

Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
            260   265   270

Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
            275   280   285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
    290   295   300

Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
305   310   315   320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
            325   330   335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
            340   345   350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
            355   360   365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
    370   375   380

Gly Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
385   390   395   400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
            405   410   415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
        420   425   430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
        435   440   445

Glu Ala Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser
    450   455   460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
465   470   475   480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
                485   490   495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
            500   505   510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
        515   520   525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
    530   535   540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
545   550   555   560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
                565   570   575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
            580   585   590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
        595   600   605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
    610   615   620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
625   630   635   640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
            645   650   655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
            660   665   670

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Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
    675                 680                 685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
    690                 695                 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
705                 710                 715                 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
            725                 730                 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
            740                 745                 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
    755                 760                 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
    770                 775                 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
785                 790                 795                 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
            805                 810                 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
            820                 825                 830

Ser Ala Lys Gly His His His His His
        835                 840
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<210> 2848

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2848
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gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac      180

gggtacaagg ccgtcttcgt ggtctttgac gccaaggccc cctccttccg ccacgaggcc      240

tacgaggcct acaaggcggg gagggccccg accccgagg acttcccccg gcagctcgcc      300

ctcatcaagg agctggtgga cctcctgggg tttacccgcc tcgaggtccc cggctacgag      360

gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc      420

atcctcaccg ccgaccgcga cctctaccaa ctcgtctccg accgcgtcgc cgtcctccac      480

cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag      540

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ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc      660

ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg      720

gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggaggtg      780

gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg      840

gagttcggca gcctcctcca cgagttcggc ctcctggagg cccccgcccc cctggaggag      900

gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccg ccccgagccc      960

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caggcccttt ccctggagct tgcggaggag atccgccgcc tcgaggagga ggtcttccgc     1440

ttggcgggcc accccttcaa cctcaactcc cgggaccagc tggaaagggt gctctttgac     1500

gagcttaggc ttcccgcctt gaagaagacg aagaagacag gcaagcgctc caccagcgcc     1560

gcggtgctgg aggccctacg ggaggcccac cccatcgtgg agaagatcct ccagcaccgg     1620

gagctcacca agctcaagaa cacctacgtg gaccccctcc caagcctcgt ccacccgagg     1680

acgggccgcc tccacacccg cttcaaccag acggccacgg ccacggggag gcttagtagc     1740

tccgacccca acctgcagaa catccccgtc cgcacccccct tgggccagag gatccgccgg     1800

gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc     1860

cgcgtcctcg cccacctctc cggggacgaa aacctgatca gggtcttcca ggagggggaag     1920
```

```
gacatccaca cccagaccgc aagctggatg ttcggcgtcc ccccggaggc cgtggacccc    1980

ctgatgcgcc gggcggccaa gacggtgaac ttcggcgtcc tctacggcat gtccgcccat    2040

aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac    2100

ttccaaagct tccccaaggt gcgggcctgg atagaaaaga ccctggagga ggggaggaag    2160

cggggctacg tggaaaccct cttcggaaga aggcgctacg tgcccgacct caacgcccgg    2220

gtgaagagcg tcagggaggc cgcggagcgc atggccttca acatgcccgt ccagggcacc    2280

gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg    2340

gcccgcatgc tcctccaggt cgccaacgag ctcctcctgg aggccccca agcgcgggcc    2400

gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc    2460

ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggtca ccaccaccac    2520

caccac                                                                2526


<210>  2849

<211>  842

<212>  PRT

<213>  Artificial Sequence


<220>

<223>  Synthetic

<400>  2849

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1               5                   10                  15


Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Arg Arg Ala Leu
                20                  25                  30


Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
        35                  40                  45


Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
    50                  55                  60


Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
65                  70                  75                  80


Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
                85                  90                  95
```

```
Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
        100             105             110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
        115             120             125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
        130             135             140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
145             150             155             160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
                165             170             175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
        180             185             190

Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
        195             200             205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
        210             215             220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
225             230             235             240

Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
                245             250             255

Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
                260             265             270

Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
        275             280             285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
        290             295             300

Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
305             310             315             320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
                325             330             335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
                340             345             350
```

```
Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
        355                 360                 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
        370                 375                 380

Gly Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
385                 390                 395                 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
                405                 410                 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
        420                 425                 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
        435                 440                 445

Glu Ala Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser
        450                 455                 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
465                 470                 475                 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
                485                 490                 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
                500                 505                 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
        515                 520                 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
        530                 535                 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
545                 550                 555                 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
                565                 570                 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
                580                 585                 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
```

```
                595                      600                      605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
    610                 615                 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
625                 630                 635                     640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
                645                 650                 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
                660                 665                 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
        675                 680                 685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
    690                 695                 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
705                 710                 715                     720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
                725                 730                 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
                740                 745                 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
        755                 760                 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
    770                 775                 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
785                 790                 795                     800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
                805                 810                 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
                820                 825                 830

Ser Ala Lys Gly His His His His His
        835                 840
```

- 2095 -

<210> 2850

<211> 2514

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2850

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ctggcctacc gcacccgctt cgccctgaag ggcctcacca ccagccgcgg ggagccggtc   120

caggcggtgt acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg   180

gtgatcgtgg tgtttgacgc caaggccccc tccttccgcc accagaccta cgaggcctac   240

aaggcggggc gggctcccac ccccgaggac tttccccggc agcttgccct tatcaaggag   300

atggtggacc ttttgggcct ggagcgcctc gaggtgccgg gctttgaagc ggatgacgtc   360

ctggctaccc tggccaagaa ggcggaaaag gaaggctacg aagtgcgcat cctcaccgcg   420

gaccgggacc tttaccagct tctttcggag cgaatctcca tccttcaccc ggagggttac   480

ctgatcaccc cggagtggct ttgggagaag tatgggctta agccttccca gtgggtggac   540

taccgggcct tggccgggga cccttccgac aacatccccg gcgtgaaggg catcggggag   600

aagacggcgg ccaagctgat ccgggagtgg ggaagcctgg aaaaccttct taagcacctg   660

gaacaggtga aacctgcctc cgtgcgggag aagatcctta gccacatgga ggacctcaag   720

ctatccctgg agctatcccg ggtgcacacg gacttgctcc ttcaggtgga cttcgcccgg   780

cgccgggagc cggaccggga ggggcttaag gccttttggg agaggctgga gttcggaagc   840

ctcctccacg agttcggcct gttggaaagc ccggtggcgg cggaggaagc tccctggccg   900

cccccccgagg gagccttcgt ggggtacgtt ctttcccgcc ccgagcccat gtgggcggag   960

cttaacgcct ggccgccgc ctggggcggc cgcgtgcacc gggcagcaga ccccttggcg  1020

gggctaaagg acctcaagga ggtccggggc ctcctcgcca aggacctcgc cgtcttggcc  1080

tcgagggagg ggctagacct cgtgcccggg acgacccca tgctcctcgc ctacctcctg  1140

ggcccctcca acaccacccc cgaggggggtg cgcggcgct acgggggggga gtggacggag  1200

gacgccgccc accgggccct cctctcggag aggctccatc ggaacctcct taagcgcctc  1260

gagggggagg agaagctcct ttggctctac cacgaggtgg aaaagcccct ctcccgggtc  1320

ctggcccaca tggaggccac cggggtacgg ctggacgtgg cctaccttca ggcccttttcc  1380

ctggagcttg cggaggagat ccgccgcctc gaggaggagg tcttccgctt ggcgggccac  1440
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- 2096 -

cccttcaacc tcaactcccg ggaccagctg gaaagggtgc tctttgacga gcttaggctt   1500

cccgccttga agaagacgaa gaagacaggc aagcgctcca ccagcgccgc ggtgctggag   1560

gccctacggg aggcccaccc catcgtggag aagatcctcc agcaccggga gctcaccaag   1620

ctcaagaaca cctacgtgga ccccctccca agcctcgtcc acccgaggac gggccgcctc   1680

cacacccgct tcaaccagac ggccacggcc acggggaggc ttagtagctc cgaccccaac   1740

ctgcagaaca tccccgtccg cacccccttg ggccagagga tccgccgggc cttcgtggcc   1800

gaggcgggtt gggcgttggt ggccctggac tatagccaga tagagctccg cgtcctcgcc   1860

cacctctccg gggacgaaaa cctgatcagg gtcttccagg aggggaagga catccacacc   1920

cagaccgcaa gctggatgtt cggcgtcccc ccggaggccg tggaccccct gatgcgccgg   1980

gcggccaaga cggtgaactt cggcgtcctc tacggcatgt ccgcccatag gctctcccag   2040

gagcttgcca tcccctacga ggaggcggtg gcctttatag agcgctactt ccaaagcttc   2100

cccaaggtgc gggcctggat agaaaagacc ctggaggagg ggaggaagcg gggctacgtg   2160

gaaaccctct tcggaagaag gcgctacgtg cccgacctca cgcccgggt gaagagcgtc   2220

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ctccaggtcg ccaacgagct cctcctggag gcccccaag cgcgggccga ggaggtggcg   2400

gctttggcca aggaggccat ggagaaggcc tatcccctcg ccgtgcccct ggaggtggag   2460

gtgggggatgg gggaggactg gctttccgcc aagggtcacc accaccacca ccac   2514

<210>   2851

<211>   838

<212>   PRT

<213>   Artificial Sequence

<220>

<223>   Synthetic

<400>   2851

Met Asn Ser Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val
1   5   10   15

Asp Gly His His Leu Ala Tyr Arg Thr Arg Phe Ala Leu Lys Gly Leu
            20   25   30

Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys

- 2097 -

Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val
    50   55   60

Phe Asp Ala Lys Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr
65   70   75   80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
                85   90   95

Leu Ile Lys Glu Met Val Asp Leu Leu Gly Leu Glu Arg Leu Glu Val
            100   105   110

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
            115   120   125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu
    130   135   140

Tyr Gln Leu Leu Ser Glu Arg Ile Ser Ile Leu His Pro Glu Gly Tyr
145   150   155   160

Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Lys Pro Ser
            165   170   175

Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile
            180   185   190

Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala Lys Leu Ile Arg
            195   200   205

Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys His Leu Glu Gln Val Lys
    210   215   220

Pro Ala Ser Val Arg Glu Lys Ile Leu Ser His Met Glu Asp Leu Lys
225   230   235   240

Leu Ser Leu Glu Leu Ser Arg Val His Thr Asp Leu Leu Leu Gln Val
            245   250   255

Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala Phe
            260   265   270

Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
    275   280   285

```
Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly
    290                 295             300

Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu
305             310             315                 320

Leu Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val His Arg Ala Ala
            325             330                 335

Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu
            340             345             350

Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val
        355             360             365

Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Gly Pro Ser Asn
    370             375             380

Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
385             390             395                 400

Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu
            405             410                 415

Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu
            420             425             430

Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly
        435             440             445

Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala
    450             455             460

Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His
465             470             475                 480

Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp
            485             490                 495

Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg
            500             505             510

Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
            515             520             525

Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr
    530             535             540
```

Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu
545   550   555   560

His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser
                565   570   575

Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln
            580   585   590

Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala
        595   600   605

Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
    610   615   620

Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr
625   630   635   640

Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro
            645   650   655

Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly
        660   665   670

Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu
    675   680   685

Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg
    690   695   700

Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val
705   710   715   720

Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg
            725   730   735

Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro
            740   745   750

Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu
        755   760   765

Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala
    770   775   780

Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala

```
           785                  790                  795                  800

           Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro
                       805                  810                  815


           Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys Gly
                       820                  825                  830


           His His His His His His
                   835


<210>   2852

<211>   2514

<212>   DNA

<213>   Artificial Sequence


<220>

<223>   Synthetic

<400>   2852
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ctggcctacc gcacccgcca cgccctgaag ggcctcacca ccagccgcgg ggagccggtc   120

caggcggtgt acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg   180

gtgatcgtgg tgtttgacgc caaggccccc tccttccgcc accagaccta cgaggcctac   240

aaggcggggc gggctcccac ccccgaggac tttccccggc agcttgccct tatcaaggag   300

atggtggacc tttttgggcct ggagcgcctc gaggtgccgg ctttgaagc ggatgacgtc   360

ctggctaccc tggccaagaa ggcggaaaag gaaggctacg aagtgcgcat cctcaccgcg   420

gaccgggacc tttaccagct tctttcggag cgaatctcca tccttcaccc ggagggttac   480

ctgatcaccc cggagtggct ttgggagaag tatgggctta gccttcccca gtgggtggac   540

taccgggcct tggccggga cccttccgac aacatccccg gcgtgaaggg catcggggag   600

aagacggcgg ccaagctgat ccgggagtgg ggaagcctgg aaaaccttct taagcacctg   660

gaacaggtga aacctgcctc cgtgcgggag aagatcctta gccacatgga ggacctcaag   720

ctatccctgg agctatcccg ggtgcacacg gacttgctcc ttcaggtgga cttcgcccgg   780

cgccgggagc cggaccggga ggggcttaag gccttttggg agaggctgga gttcggaagc   840

ctcctccacg agttcggcct gttggaaagc ccggtggcgg cggaggaagc tccctggccg   900

cccccccgagg gagccttcgt ggggtacgtt ctttcccgcc ccgagcccat gtgggcggag   960


                          - 2101 -
```

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cttaacgcct tggccgccgc ctggggcggc cgcgtgcacc gggcagcaga ccccttggcg    1020

gggctaaagg acctcaagga ggtccggggc ctcctcgcca aggacctcgc cgtcttggcc    1080

tcgagggagg ggctagacct cgtgcccggg gacgacccca tgctcctcgc ctacctcctg    1140

ggcccctcca acaccacccc cgaggggggtg gcgcggcgct acggggggga gtggacggag    1200

gacgccgccc accgggccct cctctcggag aggctccatc ggaacctcct taagcgcctc    1260

gaggggagg agaagctcct ttggctctac cacgaggtgg aaaagcccct ctcccgggtc    1320

ctggcccaca tggaggccac cggggtacgg ctggacgtgg cctaccttca ggccctttcc    1380

ctggagcttg cggaggagat ccgccgcctc gaggaggagg tcttccgctt ggcgggccac    1440

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cccgccttga agaagacgaa gaagacaggc aagcgctcca ccagcgccgc ggtgctggag    1560

gccctacggg aggcccaccc catcgtggag aagatcctcc agcaccggga gctcaccaag    1620

ctcaagaaca cctacgtgga ccccctccca agcctcgtcc acccgaggac gggccgcctc    1680

cacacccgct tcaaccagac ggccacggcc acggggaggc ttagtagctc cgaccccaac    1740

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gaggcgggtt gggcgttggt ggccctggac tatagccaga tagagctccg cgtcctcgcc    1860

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gcggccaaga cggtgaactt cggcgtcctc tacggcatgt ccgcccatag gctctcccag    2040

gagcttgcca tcccctacga ggaggcggtg gcctttatag agcgctactt ccaaagcttc    2100

cccaaggtgc gggcctggat agaaaagacc ctggaggagg ggaggaagcg gggctacgtg    2160

gaaaccctct tcggaagaag gcgctacgtg cccgacctca cgcccgggt gaagagcgtc    2220

agggaggccg cggagcgcat ggccttcaac atgcccgtcc agggcaccgc cgccgacctc    2280

atgaagctcg ccatggtgaa gctcttcccc cgcctccggg agatgggggc ccgcatgctc    2340

ctccaggtcg ccaacgagct cctcctggag gccccccaag cgcgggccga ggaggtggcg    2400

gctttggcca aggaggccat ggagaaggcc tatcccctcg ccgtgcccct ggaggtggag    2460

gtggggatgg gggaggactg gctttccgcc aagggtcacc accaccacca ccac          2514

<210>  2853

<211>  838

<212>  PRT

<213>  Artificial Sequence
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<220>

<223>   Synthetic

<400>   2853

Met Asn Ser Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val
1   5   10   15

Asp Gly His His Leu Ala Tyr Arg Thr Arg His Ala Leu Lys Gly Leu
            20   25   30

Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
        35   40   45

Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val
    50   55   60

Phe Asp Ala Lys Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr
65   70   75   80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
            85   90   95

Leu Ile Lys Glu Met Val Asp Leu Leu Gly Leu Glu Arg Leu Glu Val
            100   105   110

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
        115   120   125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu
    130   135   140

Tyr Gln Leu Leu Ser Glu Arg Ile Ser Ile Leu His Pro Glu Gly Tyr
145   150   155   160

Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Lys Pro Ser
                165   170   175

Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile
            180   185   190

Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala Lys Leu Ile Arg
        195   200   205

Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys His Leu Glu Gln Val Lys
    210   215   220

Pro Ala Ser Val Arg Glu Lys Ile Leu Ser His Met Glu Asp Leu Lys
225   230   235   240

Leu Ser Leu Glu Leu Ser Arg Val His Thr Asp Leu Leu Leu Gln Val
            245   250   255

Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala Phe
            260   265   270

Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
            275   280   285

Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly
    290   295   300

Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu
305   310   315   320

Leu Asn-Ala Leu Ala Ala Ala Trp Gly Gly Arg Val His Arg Ala Ala
            325   330   335

Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu
            340   345   350

Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val
            355   360   365

Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Gly Pro Ser Asn
    370   375   380

Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
385   390   395   400

Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu
            405   410   415

Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu
            420   425   430

Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly
    435   440   445

Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala
    450   455   460

Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His
465   470   475   480

```
Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp
            485                 490                 495

Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg
            500                 505                 510

Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
            515                 520                 525

Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr
    530                 535                 540

Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu
545                 550                 555                 560

His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser
            565                 570                 575

Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln
            580                 585                 590

Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala
    595                 600                 605

Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
    610                 615                 620

Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr
625                 630                 635                 640

Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro
            645                 650                 655

Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly
            660                 665                 670

Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu
            675                 680                 685

Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg
            690                 695                 700

Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val
705                 710                 715                 720

Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg
```

```
           725                  730                  735

Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro
        740                  745                  750


Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu
        755                  760                  765


Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala
    770                  775                  780


Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala
785                  790                  795                  800


Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro
            805                  810                  815


Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys Gly
            820                  825                  830


His His His His His His
        835


<210>   2854

<211>   2514

<212>   DNA

<213>   Artificial Sequence


<220>

<223>   Synthetic

<400>   2854
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ctggcctacc gcacccgccg cgccctgaag ggcctcacca ccagccgcgg ggagccggtc     120

caggcggtgt acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg     180

gtgatcgtgg tgtttgacgc caaggccccc tccttccgcc accagaccta cgaggcctac     240

aaggcggggc gggctcccac ccccgaggac tttccccggc agcttgccct tatcaaggag     300

atggtggacc ttttgggcct ggagcgcctc gaggtgccgg ctttgaagc ggatgacgtc     360

ctggctaccc tggccaagaa ggcggaaaag gaaggctacg aagtgcgcat cctcaccgcg     420

gaccgggacc tttaccagct tctttcggag cgaatctcca tccttcaccc ggagggttac     480
```

```
ctgatcaccc cggagtggct ttgggagaag tatgggctta agccttccca gtgggtggac     540

taccgggcct tggccgggga cccttccgac aacatccccg gcgtgaaggg catcggggag     600

aagacggcgg ccaagctgat ccgggagtgg ggaagcctgg aaaaccttct taagcacctg     660

gaacaggtga aacctgcctc cgtgcgggag aagatcctta gccacatgga ggacctcaag     720

ctatccctgg agctatcccg ggtgcacacg gacttgctcc ttcaggtgga cttcgcccgg     780

cgccgggagc cggaccggga ggggcttaag gccttttttgg agaggctgga gttcggaagc     840

ctcctccacg agttcggcct gttggaaagc ccggtggcgg cggaggaagc tccctggccg     900

ccccccgagg gagccttcgt ggggtacgtt ctttcccgcc ccgagcccat gtgggcggag     960

cttaacgcct tggccgccgc ctggggcggc cgcgtgcacc gggcagcaga ccccttggcg    1020

gggctaaagg acctcaagga ggtccggggc ctcctcgcca aggacctcgc cgtcttggcc    1080

tcgagggagg ggctagacct cgtgcccggg gacgacccca tgctcctcgc ctacctcctg    1140

ggcccctcca acaccacccc cgaggggggtg gcgcggcgct acggggggga gtggacggag    1200

gacgccgccc accgggccct cctctcggag aggctccatc ggaacctcct taagcgcctc    1260

gaggggggagg agaagctcct ttggctctac cacgaggtgg aaaagcccct ctcccgggtc    1320

ctggcccaca tggaggccac cggggtacgg ctggacgtgg cctaccttca ggcccttttcc    1380

ctggagcttg cggaggagat ccgccgcctc gaggaggagg tcttccgctt ggcgggccac    1440

cccttcaacc tcaactcccg ggaccagctg gaaagggtgc tctttgacga gcttaggctt    1500

cccgccttga agaagacgaa gaagacaggc aagcgctcca ccagcgccgc ggtgctggag    1560

gccctacggg aggcccaccc catcgtggag aagatcctcc agcaccggga gctcaccaag    1620

ctcaagaaca cctacgtgga cccccctccca agcctcgtcc acccgaggac gggccgcctc    1680

cacacccgct tcaaccagac ggccacggcc acggggaggc ttagtagctc cgaccccaac    1740

ctgcagaaca tccccgtccg cacccccttg ggccagagga tccgccgggc cttcgtggcc    1800

gaggcgggtt gggcgttggt ggccctggac tatagccaga tagagctccg cgtcctcgcc    1860

cacctctccg gggacgaaaa cctgatcagg gtcttccagg aggggaagga catccacacc    1920

cagaccgcaa gctggatgtt cggcgtcccc ccggaggccg tggaccccct gatgcgccgg    1980

gcggccaaga cggtgaactt cggcgtcctc tacggcatgt ccgcccatag gctctcccag    2040

gagcttgcca tcccctacga ggaggcggtg gcctttatag agcgctactt ccaaagcttc    2100

cccaaggtgc gggcctggat agaaaagacc ctggaggagg ggaggaagcg gggctacgtg    2160

gaaaccctct tcggaagaag gcgctacgtg cccgacctca acgcccgggt gaagagcgtc    2220

agggaggccg cggagcgcat ggccttcaac atgcccgtcc agggcaccgc cgccgacctc    2280

atgaagctcg ccatggtgaa gctcttcccc cgcctccggg agatgggggc ccgcatgctc    2340
```

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ctccaggtcg ccaacgagct cctcctggag gcccccaag cgcgggccga ggaggtggcg    2400

gctttggcca aggaggccat ggagaaggcc tatcccctcg ccgtgcccct ggaggtggag    2460

gtggggatgg gggaggactg gctttccgcc aagggtcacc accaccacca ccac          2514
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<210> 2855

<211> 838

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2855

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Met Asn Ser Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val
1               5               10                  15


Asp Gly His His Leu Ala Tyr Arg Thr Arg Arg Ala Leu Lys Gly Leu
            20              25                  30


Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
        35              40                  45


Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val
    50              55                  60


Phe Asp Ala Lys Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr
65              70              75                  80


Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
                85              90                  95


Leu Ile Lys Glu Met Val Asp Leu Leu Gly Leu Glu Arg Leu Glu Val
            100             105                 110


Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
        115             120                 125


Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu
    130             135                 140


Tyr Gln Leu Leu Ser Glu Arg Ile Ser Ile Leu His Pro Glu Gly Tyr
145             150             155                 160
```

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```
Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Lys Pro Ser
            165                 170             175


Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile
            180                 185             190


Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala Lys Leu Ile Arg
            195                 200             205


Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys His Leu Glu Gln Val Lys
    210                 215                 220


Pro Ala Ser Val Arg Glu Lys Ile Leu Ser His Met Glu Asp Leu Lys
225                 230                 235                 240


Leu Ser Leu Glu Leu Ser Arg Val His Thr Asp Leu Leu Leu Gln Val
            245                 250             255


Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala Phe
            260                 265             270


Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
            275                 280             285


Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly
    290                 295                 300


Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu
305                 310                 315                 320


Leu Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val His Arg Ala Ala
            325                 330             335


Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu
            340                 345             350


Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val
            355                 360             365


Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Gly Pro Ser Asn
    370                 375                 380


Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
385                 390                 395                 400


Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu
            405                 410             415
```

Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu
        420   425   430

Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly
        435   440   445

Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala
        450   455   460

Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His
465   470   475   480

Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp
                485   490   495

Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg
        500   505   510

Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
        515   520   525

Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr
        530   535   540

Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu
545   550   555   560

His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser
                565   570   575

Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln
                580   585   590

Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala
        595   600   605

Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
        610   615   620

Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr
625   630   635   640

Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro
                645   650   655

Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly

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Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu
        675   680   685

Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg
        690   695   700

Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val
705   710   715   720

Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg
                725   730   735

Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro
            740   745   750

Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu
        755   760   765

Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala
    770   775   780

Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala
785   790   795   800

Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro
                805   810   815

Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys Gly
            820   825   830

His His His His His His
        835

<210>   2856

<211>   2517

<212>   DNA

<213>   Artificial Sequence

<220>

<223>   Synthetic

<400>   2856

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ccggtgcagg cggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg     180

gacgcggtga tcgtggtctt tgacgccaag gccccctcct ccgccacga ggcctacggg      240

gggtacaagg cgggccgggc ccccacgccg gaggactttc cccggcaact cgccctcatc     300

aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac     360

gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg ctacgaggt ccgcatcctc      420

accgccgaca agacccttta ccagctcctt ccgaccgca tccacgtcct ccaccccgag      480

gggtacctca tcaccccggc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg     540

gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggt caagggcatc     600

ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag     660

aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg     720

aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc     780

aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc     840

agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg     900

cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc     960

gatcttctgg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agacccctlg    1020

gcggggctaa aggacctcaa ggaggtccgg ggcctcctcg ccaaggacct cgccgtcttg    1080

gcctcgaggg aggggctaga cctcgtgccc ggggacgacc ccatgctcct cgcctacctc    1140

ctgggcccct ccaacaccac ccccgagggg gtggcgcggc gctacggggg ggagtggacg    1200

gaggacgccg cccaccgggc cctcctctcg gagaggctcc atcggaacct ccttaagcgc    1260

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cttcccgcct tgaagaagac gaagaagaca ggcaagcgct ccaccagcgc cgcggtgctg    1560

gaggccctac gggaggccca ccccatcgtg gagaagatcc tccagcaccg ggagctcacc    1620

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ctccacaccc gcttcaacca gacggccacg gccacgggga ggcttagtag ctccgacccc    1740

aacctgcaga acatccccgt ccgcacccccc ttgggccaga ggatccgccg ggccttcgtg    1800

gccgaggcgg gttgggcgtt ggtggccctg gactatagcc agatagagct ccgcgtcctc    1860
```

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gcccacctct ccggggacga aaacctgatc agggtcttcc aggaggggaa ggacatccac      1920

acccagaccg caagctggat gttcggcgtc cccccggagg ccgtggaccc cctgatgcgc      1980

cgggcggcca agacggtgaa cttcggcgtc ctctacggca tgtccgccca taggctctcc      2040

caggagcttg ccatcccta cgaggaggcg gtggccttta tagagcgcta cttccaaagc       2100

ttccccaagg tgcgggcctg gatagaaaag accctggagg aggggaggaa gcggggctac      2160

gtggaaaccc tcttcggaag aaggcgctac gtgcccgacc tcaacgcccg ggtgaagagc      2220

gtcagggagg ccgcggagcg catggccttc aacatgcccg tccagggcac cgccgccgac      2280

ctcatgaagc tcgccatggt gaagctcttc ccccgcctcc gggagatggg ggcccgcatg      2340

ctcctccagg tcgccaacga gctcctcctg gaggcccccc aagcgcgggc cgaggaggtg      2400

gcggctttgg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggaggtg      2460

gaggtggggga tgggggagga ctggctttcc gccaagggtc accaccacca ccaccac       2517
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<210> 2857

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2857

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Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1               5                   10                  15


Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Arg His Ala Leu Lys
                20                  25                  30


Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
            35                  40                  45


Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
        50                  55                  60


Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65                  70                  75                  80


Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
                85                  90                  95
```

```
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
            100                 105                 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
            115                 120                 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
        130                 135                 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145                 150                 155                 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
                165                 170                 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
            180                 185                 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
            195                 200                 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
        210                 215                 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
225                 230                 235                 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
                245                 250                 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
            260                 265                 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
        275                 280                 285

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
        290                 295                 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
305                 310                 315                 320

Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
            325                 330                 335

Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
            340                 345                 350
```

Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
        355   360   365

Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Gly Pro Ser
        370   375   380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
385   390   395   400

Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
                405   410   415

Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
                420   425   430

Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
        435   440   445

Gly Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
        450   455   460

Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
465   470   475   480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
                485   490   495

Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys
                500   505   510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
        515   520   525

Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
        530   535   540

Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
545   550   555   560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
                565   570   575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
                580   585   590

Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val

```
                595                      600                      605

Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
    610                 615                 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His
625                 630                 635                     640

Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp
                645                 650                     655

Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr
            660                 665                 670

Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
            675                 680                 685

Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
    690                 695                 700

Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr
705                 710                 715                     720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala
                725                 730                 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
            740                 745                 750

Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
            755                 760                 765

Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val
    770                 775                 780

Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val
785                 790                 795                     800

Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val
                805                 810                     815

Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys
            820                 825                 830

Gly His His His His His His
    835
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<210> 2858

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2858
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<210> 2859

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2859
ggtggtgttc gaagggtcca ggaggtaggc g   31

<210> 2860

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2860
ggtacggcgg gacgtggcct accttcag   28

<210> 2861

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2861
ctgaaggtag gccacgtccc gccgtacc   28

<210> 2862

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2862
cacctggcct accgcacccg cttcgccctg aagggcctc   39

<210> 2863

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2863
gaggcccttc agggcgaagc gggtgcggta ggccaggtg   39

<210> 2864

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2864
cacctggcct accgcacccg ccacgccctg aagggcctca cc   42

<210> 2865

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2865
ggtgaggccc ttcagggcgt ggcgggtgcg gtaggccagg tg   42

<210> 2866

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2866
cacctggcct accgcacccg ccgcgccctg aagggcctca cc   42

<210> 2867

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2867
ggtgaggccc ttcagggcgc ggcgggtgcg gtaggccagg tg   42

<210> 2868

<211> 13

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (3)..(3)

<223> The residue at this position is linked to a Z28 quenching group.

<400> 2868
cactgcttcg tgg   13

<210> 2869

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

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